

```

Matches      5;  Conservative      1;  Mismatches      2;  Indels      0;  Gaps      0;

QY      2 FPDENFKL 9
DB      1 FPDKKHKL 8

RESULT 37
ABJ43122
ID      ABJ43122 standard; peptide; 9 AA.
XX
AC      ABJ43122;
XX
DT      17-OCT-2003 (first entry)
XX
DE      151P3D4 cancer gene related HLA peptide #942.
XX
KW      Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW      cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW      bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS      Homo sapiens.
XX
PN      WO200283860-A2.
XX
PD      24-OCT-2002.
XX
PF      09-APR-2002; 2002WO-US011644.
XX
PR      10-APR-2001; 2001US-0282739P.
PR      25-APR-2001; 2001US-0286630P.
XX
PA      (AGEN-) AGENSYS INC.
XX
PI      Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI      Morrison RK, Ge W, Jakobovits A;
XX
DR      WPI; 2003-167091/16.
XX
PT      New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT      cellular immune response, or for diagnosing, prognosing, preventing or
PT      treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT      or carcinoma.
XX
PS      Claim 13; Page 167; 426pp; English.
XX
CC      The invention relates to a novel composition comprising a substance that
CC      modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC      a molecule that is modulated by the 151P3D4 protein, where the status of
CC      a cell that expresses the 151P3D4 protein is modulated. The novel
CC      compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC      a humoral or cellular immune response. The 151P3D4 genes and proteins
CC      are also useful for diagnosing, prognosing, preventing or treating
CC      cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC      bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC      human leukocyte antigen peptide relating to the 151P3D4 composition of
CC      the invention
XX
SQ      Sequence 9 AA;

Query Match      56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches      5;  Conservative      1;  Mismatches      2;  Indels      0;  Gaps      0;

QY      2 FPDENFKL 9
DB      1 FPDKKHKL 8

RESULT 38
ABJ46322
ID      ABJ46322 standard; peptide; 9 AA.
XX

```

```

AC      ABJ46322;
XX
DT      16-OCT-2003 (first entry)
XX
DE      151P3D4 cancer gene related HLA peptide #4142.
XX
KW      Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW      cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW      bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS      Homo sapiens.
XX
PN      WO200283860-A2.
XX
PD      24-OCT-2002.
XX
PF      09-APR-2002; 2002WO-US011644.
XX
PR      10-APR-2001; 2001US-0282739P.
PR      25-APR-2001; 2001US-0286630P.
XX
PA      (AGEN-) AGENSYS INC.
XX
PI      Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
PI      Morrison RK, Ge W, Jakobovits A;
XX
DR      WPI; 2003-167091/16.
XX
PT      New 151P3D4 proteins and genes, useful for eliciting a humoral or
PT      cellular immune response, or for diagnosing, prognosing, preventing or
PT      treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
PT      or carcinoma.
XX
PS      Claim 13; Page 198; 426pp; English.
XX
CC      The invention relates to a novel composition comprising a substance that
CC      modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
CC      a molecule that is modulated by the 151P3D4 protein, where the status of
CC      a cell that expresses the 151P3D4 protein is modulated. The novel
CC      compositions, or the 151P3D4 proteins and genes, are useful for eliciting
CC      a humoral or cellular immune response. The 151P3D4 genes and proteins
CC      are also useful for diagnosing, prognosing, preventing or treating
CC      cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
CC      bronchial cancer, breast cancer or carcinoma. This sequence represents a
CC      human leukocyte antigen peptide relating to the 151P3D4 composition of
CC      the invention
XX
SQ      Sequence 9 AA;

Query Match      56.0%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches      5;  Conservative      1;  Mismatches      2;  Indels      0;  Gaps      0;

QY      2 FPDENFKL 9
DB      2 FPDKKHKL 9

RESULT 39
ABJ47111
ID      ABJ47111 standard; peptide; 9 AA.
XX
AC      ABJ47111;
XX
DT      16-OCT-2003 (first entry)
XX
DE      151P3D4 cancer gene related HLA peptide #4931.
XX
KW      Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
KW      cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW      bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
OS      Homo sapiens.

```

```
XX WO200283860-A2.
XX 24-OCT-2002.
XX
XX 09-APR-2002; 2002WO-US011644.
XX
XX 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX Claim 13; Page 206; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX a molecule that is modulated by the 151P3D4 protein, where the status of
XX a cell that expresses the 151P3D4 protein is modulated. The novel
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX a humoral or cellular immune response. The 151P3D4 genes and proteins
XX are also useful for diagnosing, prognosing, preventing or treating
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX human leukocyte antigen peptide relating to the 151P3D4 composition of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 FPDENFKL 9
XX |||: ||
XX Db 1 FPDKKHKL 8
XX
XX
XX RESULT 40
XX ABJ48392
XX ID ABJ48392 standard; peptide; 9 AA.
XX AC ABJ48392;
XX
XX DT 16-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related HLA peptide #6212.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
XX OS Homo sapiens.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX Claim 13; Page 206; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX a molecule that is modulated by the 151P3D4 protein, where the status of
XX a cell that expresses the 151P3D4 protein is modulated. The novel
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX a humoral or cellular immune response. The 151P3D4 genes and proteins
XX are also useful for diagnosing, prognosing, preventing or treating
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX human leukocyte antigen peptide relating to the 151P3D4 composition of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 FPDENFKL 9
XX |||: ||
XX Db 1 FPDKKHKL 8
XX
XX
XX RESULT 41
XX ABJ39852
XX ID ABJ39852 standard; peptide; 9 AA.
XX AC ABJ39852;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related peptide #479.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX bronchial; breast; carcinoma.
XX
XX OS Unidentified.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX (AGEN-) AGENSYS INC.
```

```
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX Claim 13; Page 218; 426pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX a molecule that is modulated by the 151P3D4 protein, where the status of
XX a cell that expresses the 151P3D4 protein is modulated. The novel
XX compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX a humoral or cellular immune response. The 151P3D4 genes and proteins
XX are also useful for diagnosing, prognosing, preventing or treating
XX cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX human leukocyte antigen peptide relating to the 151P3D4 composition of
XX the invention
XX
XX Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 RPDENFKL 9
XX |||: ||
XX Db 2 FPDKKHKL 9
XX
XX
XX RESULT 41
XX ABJ39852
XX ID ABJ39852 standard; peptide; 9 AA.
XX AC ABJ39852;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related peptide #479.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX bronchial; breast; carcinoma.
XX
XX OS Unidentified.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX
XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX Morrison RK, Ge W, Jakobovits A;
XX WPI; 2003-167091/16.
XX
XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX cellular immune response, or for diagnosing, prognosing, preventing or
XX treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX or carcinoma.
XX
XX (AGEN-) AGENSYS INC.
```

PS Claim 13; Page 131; 426pp; English.

XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosing, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC 151P3D4 related peptide of the invention

XX Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
 Db 2 FPDKKHKL 9
 |||: ||

RESULT 42

ABJ41450
 ID ABJ41450 standard; peptide; 9 AA.
 AC ABJ41450;
 XX
 XX 17-OCT-2003 (first entry)

DE 151P3D4 cancer gene related peptide #2077.

XX Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
 KW bronchial; breast; carcinoma.
 XX Unidentified.
 OS
 XX WO200283860-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US011644.
 PF
 XX 10-APR-2001; 2001US-0282739P.
 PR
 XX 25-APR-2001; 2001US-0286630P.
 PP
 XX (AGEN-) AGENSYS INC.
 PA
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
 PI Morrison RK, Ge W, Jakobovits A;
 PI
 XX WPI; 2003-167091/16.
 DR
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
 PT cellular immune response, or for diagnosing, prognosing, preventing or
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
 PT or carcinoma.
 PT
 XX Claim 13; Page 147; 426pp; English.

XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosing, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC 151P3D4 related peptide of the invention

XX Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
 Db 1 FPDKKHKL 8
 |||: ||

RESULT 43

ABJ46607
 ID ABJ46607 standard; peptide; 9 AA.
 XX
 AC ABJ46607;
 XX
 XX 16-OCT-2003 (first entry)

DE 151P3D4 cancer gene related HLA peptide #4427.

XX Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
 KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
 KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
 XX Homo sapiens.
 OS
 XX WO200283860-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US011644.
 PF
 XX 10-APR-2001; 2001US-0282739P.
 PR
 XX 25-APR-2001; 2001US-0286630P.
 PP
 XX (AGEN-) AGENSYS INC.
 PA
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
 PI Morrison RK, Ge W, Jakobovits A;
 PI
 XX WPI; 2003-167091/16.
 DR
 XX New 151P3D4 proteins and genes, useful for eliciting a humoral or
 PT cellular immune response, or for diagnosing, prognosing, preventing or
 PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
 PT or carcinoma.
 PT
 XX Claim 13; Page 201; 426pp; English.

XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
 CC a molecule that is modulated by the 151P3D4 protein, where the status of
 CC a cell that expresses the 151P3D4 protein is modulated. The novel
 CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
 CC a humoral or cellular immune response. The 151P3D4 genes and proteins
 CC are also useful for diagnosing, prognosing, preventing or treating
 CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
 CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
 CC human leukocyte antigen peptide relating to the 151P3D4 composition of
 CC the invention
 CC

XX Sequence 9 AA;

Query Match 56.0%; Score 28; DB 6; Length 9;
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FPDENFKL 9
 Db 1 FPDKKHKL 8
 |||: ||

```

RESULT 44
ABJ40977
ID ABJ40977 standard; peptide; 9 AA.
XX
XX AC ABJ40977;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related peptide #1604.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX KW bronchial; breast; carcinoma.
XX
XX OS Unidentified.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;
XX PR cellular immune response; adenocarcinoma; bladder; colorectal; lung;
XX PR bronchial; breast; carcinoma.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX PI Morrison RK, Ge W, Jakobovits A;
XX
XX DR WPI; 2003-167091/16.
XX
XX PT New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX PT cellular immune response, or for diagnosing, prognosing, preventing or
XX PT treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX PT or carcinoma.
XX
XX PS Claim 13; Page 143; 426pp; English.
XX
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX CC a molecule that is modulated by the 151P3D4 protein, where the status of
XX CC a cell that expresses the 151P3D4 protein is modulated. The novel
XX CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX CC a humoral or cellular immune response. The 151P3D4 genes and proteins
XX CC are also useful for diagnosing, prognosing, preventing or treating
XX CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX CC 151P3D4 related peptide of the invention
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 2 FPDENFKL 9
XX |||: ||
XX Db 2 FPDKKHKL 9
XX

RESULT 45
ABJ49160
ID ABJ49160 standard; peptide; 9 AA.
XX
XX AC ABJ49160;
XX
XX DT 16-OCT-2003 (first entry)
XX
XX DE 151P3D4 cancer gene related HLA peptide #6980.
XX
XX KW Cytostatic; gene therapy; vaccine; modulator; 151P3D4; humoral; cancer;

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```

KW cellular immune response; adenocarcinoma; bladder; colorectal; lung;
KW bronchial; breast; carcinoma; human leukocyte antigen; HLA.
XX
XX OS Homo sapiens.
XX
XX PN WO200283860-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US011644.
XX
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 25-APR-2001; 2001US-0286630P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison K;
XX PI Morrison RK, Ge W, Jakobovits A;
XX
XX DR WPI; 2003-167091/16.
XX
XX PF New 151P3D4 proteins and genes, useful for eliciting a humoral or
XX PF cellular immune response, or for diagnosing, prognosing, preventing or
XX PF treating cancer, e.g. adenocarcinoma, bladder cancer, lung, breast cancer
XX PF or carcinoma.
XX
XX PS Claim 13; Page 225; 426pp; English.
XX
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a 151P3D4 protein (e.g. 151P3D4 variant 1-11; or
XX CC a molecule that is modulated by the 151P3D4 protein, where the status of
XX CC a cell that expresses the 151P3D4 protein is modulated. The novel
XX CC compositions, or the 151P3D4 proteins and genes, are useful for eliciting
XX CC a humoral or cellular immune response. The 151P3D4 genes and proteins
XX CC are also useful for diagnosing, prognosing, preventing or treating
XX CC cancer, e.g. adenocarcinoma, bladder cancer, colorectal cancer, lung or
XX CC bronchial cancer, breast cancer or carcinoma. This sequence represents a
XX CC human leukocyte antigen peptide relating to the 151P3D4 composition of
XX CC the invention
XX
XX SQ Sequence 9 AA;
XX
XX Query Match 56.0%; Score 28; DB 6; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 2 FPDENFKL 9
XX |||: ||
XX Db 2 FPDKKHKL 9
XX

Search completed: August 30, 2004, 10:49:35
Job time : 15.4088 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 8.66554 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	53.4	9	4	Q9H326 homo sapien
2	26	44.8	10	11	Q9QVE9 mus sp. pro
3	24	41.4	9	13	Q9PRJ4 lepisosteus
4	24	41.4	12	15	O12090 caprine art
5	24	41.4	12	15	O12094 caprine art
6	24	41.4	12	15	O12114 caprine art
7	24	41.4	12	15	O12082 caprine art
8	24	41.4	12	15	O12106 caprine art
9	24	41.4	12	15	O12092 caprine art
10	24	41.4	12	15	O12108 caprine art
11	24	41.4	12	15	O12074 caprine art
12	24	41.4	12	15	O12116 caprine art
13	24	41.4	12	15	O12118 caprine art
14	24	41.4	12	15	O12110 caprine art
15	24	41.4	12	15	O12112 caprine art
16	24	41.4	12	15	O12076 caprine art

17	24	41.4	12	15	O12088	O12088 caprine art
18	24	41.4	12	15	O12078	O12078 caprine art
19	24	41.4	12	15	O12080	O12080 caprine art
20	24	41.4	12	15	O12084	O12084 caprine art
21	24	41.4	12	15	O12086	O12086 caprine art
22	22	37.9	12	7	O77915	O77915 oreochromis
23	21	36.2	8	6	O9TRY3	O9TRY3 sus sp. ins
24	21	36.2	12	10	Q93YC8	Q93YC8 nicotiana t
25	21	36.2	14	2	Q9RSP6	Q9RSP6 legionella
26	21	36.2	14	5	O18502	O18502 schistosoma
27	20	34.5	14	7	O8MH06	O8MH06 homo sapien
28	20	34.5	14	7	O8MH35	O8MH35 homo sapien
29	20	34.5	14	7	O8MH39	O8MH39 homo sapien
30	20	34.5	14	7	O8MH18	O8MH18 homo sapien
31	20	34.5	14	7	O8MH55	O8MH55 homo sapien
32	20	34.5	14	7	O8MH40	O8MH40 homo sapien
33	20	34.5	14	7	O8MH07	O8MH07 homo sapien
34	20	34.5	14	7	O8MH04	O8MH04 homo sapien
35	20	34.5	14	7	O8MH52	O8MH52 homo sapien
36	20	34.5	14	7	O8MH26	O8MH26 homo sapien
37	20	34.5	14	7	O8MH53	O8MH53 homo sapien
38	20	34.5	14	7	O8MH20	O8MH20 homo sapien
39	20	34.5	14	7	O8MH27	O8MH27 homo sapien
40	20	34.5	14	7	O8MH05	O8MH05 homo sapien
41	20	34.5	14	7	O8MH16	O8MH16 homo sapien
42	20	34.5	14	7	O8MH38	O8MH38 homo sapien
43	20	34.5	14	7	O8MH56	O8MH56 homo sapien
44	20	34.5	14	7	O8MH14	O8MH14 homo sapien
45	20	34.5	14	7	O8MH31	O8MH31 homo sapien

ALIGNMENTS

RESULT 1

Q9H326 PRELIMINARY; PRT; 9 AA.
AC Q9H326;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit (Fragment).
DE IDH3A.
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;
RT "Structural and functional characterization of the human NAD+-dependent isocitrate dehydrogenase alpha subunit promoter."
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAC43379.1; -.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 53.4%; Score 31; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWVS 8
|||
Db 3 GPAWIS 8

RESULT 2

Q9QVE9 PRELIMINARY; PRT; 10 AA.
AC Q9QVE9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

```
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/11 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
RT processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1029 MW; FCAD2DD8676866D1 CRC64;

Query Match 44.8%; Score 26; DB 11; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 5
DB 3 HQPG 7

RESULT 3
Q9PRJ4 PRELIMINARY; PRT; 9 AA.
AC Q9PRJ4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Bradykinin.
OS Lepisosteus osseus (Long-nosed gar), and
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Semionotiformes; Lepisosteidae;
OC Lepisosteus
OX NCBI_TaxID=34771, 7924;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489(1995).
SQ SEQUENCE 9 AA; 1099 MW; 3393D775A3786777 CRC64;

Query Match 41.4%; Score 24; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 3 PGW 5

RESULT 4
O12090 PRELIMINARY; PRT; 12 AA.
AC O12090;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tat protein (fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

RESULT 5
O12094 PRELIMINARY; PRT; 12 AA.
AC O12094;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tat protein (fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81438; AAB60830.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

RESULT 6
O12114 PRELIMINARY; PRT; 12 AA.
AC O12114;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Tat protein (fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
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RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81448; AAB60850.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 7
O12082 PRELIMINARY; PRT; 12 AA.
AC O12082;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81432; AAB60818.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 8
O12106 PRELIMINARY; PRT; 12 AA.
AC O12106;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81444; AAB60842.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 9
O12092 PRELIMINARY; PRT; 12 AA.
AC O12092;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81437; AAB60828.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;
Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PGW 6
Db 8 PGW 10
RESULT 10
O12108 PRELIMINARY; PRT; 12 AA.
AC O12108;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81445; AAB60844.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; LentiViral_Tat.
DR Pfam; PF02998; LentiViral_Tat; I.

```

FT NON TER 1 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

RESULT 11
O12074 PRELIMINARY; PRT; 12 AA.
AC O12074;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81428; AAB60810.1; -.
DR GO; GO:0016563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

RESULT 12
O12116 PRELIMINARY; PRT; 12 AA.
AC O12116;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81449; AAB60852.1; -.
DR GO; GO:0016563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

RESULT 13
O12118 PRELIMINARY; PRT; 12 AA.
AC O12118;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81450; AAB60854.1; -.
DR GO; GO:0016563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

RESULT 14
O12110 PRELIMINARY; PRT; 12 AA.
AC O12110;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81446; AAB60846.1; -.
DR GO; GO:0016563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
DB 8 PGW 10

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QY 4 PGW 6
|
|
|
Db 8 PGW 10

RESULT 15
O12112 PRELIMINARY; PRT; 12 AA.
ID O12112; 1997 (TrEMBLrel. 04, Created)
AC O12112; 1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81447; AAB60848.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
|
|
|
Db 8 PGW 10

RESULT 16
O12076 PRELIMINARY; PRT; 12 AA.
ID O12076; 1997 (TrEMBLrel. 04, Created)
AC O12076; 1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81429; AAB60812.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
|
|
|
Db 8 PGW 10

Db 8 PGW 10

RESULT 17
O12088 PRELIMINARY; PRT; 12 AA.
ID O12088; 1997 (TrEMBLrel. 04, Created)
AC O12088; 1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81435; AAB60824.1; -.
FT NON TER 1
SQ SEQUENCE 12 AA; 1279 MW; 4B90BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
|
|
|
Db 8 PGW 10

RESULT 18
O12078 PRELIMINARY; PRT; 12 AA.
ID O12078; 1997 (TrEMBLrel. 04, Created)
AC O12078; 1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81430; AAB60814.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
|
|
|
Db 8 PGW 10

RESULT 19
O12080 PRELIMINARY; PRT; 12 AA.
ID O12080; 1997 (TrEMBLrel. 04, Created)
AC O12080; 1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81430; AAB60814.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; 1.
FT NON TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
|
|
|
Db 8 PGW 10

```

DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81431; AAB60816.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PGW 6
Db 8 PGW 10

RESULT 20
O12084 PRELIMINARY; PRT; 12 AA.
AC O12084;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81433; AAB60820.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PGW 6
Db 8 PGW 10

RESULT 21
O12086 PRELIMINARY; PRT; 12 AA.
AC O12086;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE Tat protein (Fragment).
GN TAT.
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11660;
RN [1]
RP SEQUENCE FROM N.A.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G
to A substitutions.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81434; AAB60822.1; -.
DR GO; GO:0016563; F:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02998; Lentiviral_Tat; I.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1E8644EB7 CRC64;

Query Match 41.4%; Score 24; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PGW 6
Db 8 PGW 10

RESULT 22
O77915 PRELIMINARY; PRT; 12 AA.
AC O77915;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050028; AAC41367.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1426 MW; 9D2F47DB7A787045 CRC64;

Query Match 37.9%; Score 22; DB 7; Length 12;
Best Local Similarity 40.0%; Pred. No. 3.6e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GWVSM 9
Db 7 GWIAV 11

RESULT 23
QSTRY3 PRELIMINARY; PRT; 8 AA.
AC QSTRY3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS Sus sp.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9826;
RN [1]
RP SEQUENCE.

RX MEDLINE=92049376; PubMed=1719383;
RA Shimazaki S., Gao L., Shimonaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
protein-6";
RL Mol. Endocrinol. 5:938-948(1991).
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;

Query Match 36.2%; Score 21; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
Db 2 GPCW 5

RESULT 24

Q93YC8 PRELIMINARY; PRT; 12 AA.
AC Q93YC8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative coat protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA van der Winden J.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20027532; PubMed=10557305;
RA Jakowitsch J., Mette M.F., van der Winden J., Matzke M.A.,
RA Matzke A.J.;
RT "Integrated pararetroviral sequences define a unique class of
dispersed repetitive DNA in plants";
RT Proc. Natl. Acad. Sci. U.S.A. 96:13241-13246(1999).
DR EMBL; AJ414170; CAC88799.1;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1402 MW; 89226B3A0351E321 CRC64;

Query Match 36.2%; Score 21; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVG 3
Db 7 HVG 9

RESULT 25

Q9R5P6 PRELIMINARY; PRT; 14 AA.
AC Q9R5P6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Major outer membrane protein 31 kDa subunit, MOMP 31 kDa subunit
(Fragment).

OS Legionella pneumophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE.

RX MEDLINE=92121130; PubMed=1310095;
RA Hoffman P.S., Seyer J.H., Butler C.A.;
RT "Molecular characterization of the 28- and 31-kilodalton subunits of
the Legionella pneumophila major outer membrane protein";
RL J. Bacteriol. 174:908-913(1992).
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1490 MW; 3541B0FB1AF55F48 CRC64;

Query Match 36.2%; Score 21; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
Db 1 GPCW 4

RESULT 26

O18502 PRELIMINARY; PRT; 14 AA.
AC O18502;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lysophospholipase homolog (Fragment).
GN SMPPLH.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Egyptian;
RX MEDLINE=99011094; PubMed=9797070;
RA Hamdan F.F., Ribeiro P.;
RT "Cloning and sequence analysis of a lysophospholipase homologue from
Schistosoma mansoni";
RL Parasitol. Res. 84:839-842(1998).
DR EMBL; AF006679; AAC62255.1;
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1541 MW; 48B847C2E5D89177 CRC64;

Query Match 36.2%; Score 21; DB 5; Length 14;
Best Local Similarity 75.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
Db 11 GPCW 14

RESULT 27

Q8MH06 PRELIMINARY; PRT; 14 AA.
AC Q8MH06;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533934; AAM94848.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 28
Q8MH35 ID Q8MH35 PRELIMINARY; PRT; 14 AA.
AC Q8MH35;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533905; AAM94819.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 29
Q8MH39 ID Q8MH39 PRELIMINARY; PRT; 14 AA.
AC Q8MH39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533901; AAM94815.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 30
Q8MH18 ID Q8MH18 PRELIMINARY; PRT; 14 AA.
AC Q8MH18;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533922; AAM94836.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPG 4
Db 10 HQGP 13

RESULT 31
Q8MH55 ID Q8MH55 PRELIMINARY; PRT; 14 AA.
AC Q8MH55;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
 RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
 RT and polyadenylation of the 3' UTR."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF515808; AAM74915.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;
 Query Match 34.5%; Score 20; DB 7; Length 14;
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HYGP 4
 Db 10 HQGP 13
 RESULT 32
 Q8MH40
 ID Q8MH40 PRELIMINARY; PRT; 14 AA.
 AC Q8MH40;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533900; AAM94814.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;
 Query Match 34.5%; Score 20; DB 7; Length 14;
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HYGP 4
 Db 10 HQGP 13
 RESULT 33
 Q8MH07
 ID Q8MH07 PRELIMINARY; PRT; 14 AA.
 AC Q8MH07;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533933; AAM94847.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;
 Query Match 34.5%; Score 20; DB 7; Length 14;
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HYGP 4
 Db 10 HQGP 13
 RESULT 34
 Q8MH04
 ID Q8MH04 PRELIMINARY; PRT; 14 AA.
 AC Q8MH04;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE MHC class II antigen (Fragment).
 GN HLA-DQA1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
 RT "A new splicing acceptor site and polyadenylation sequence signal
 RT contribute to increase the extraordinary diversity of DQA1 mRNA
 RT isoforms."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF533936; AAM94850.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;
 Query Match 34.5%; Score 20; DB 7; Length 14;
 Best Local Similarity 75.0%; Pred. No. 8.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HYGP 4
 Db 10 HQGP 13
 RESULT 35
 Q8MH52

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ID Q8MH52 PRELIMINARY; PRT; 14 AA.
AC Q8MH53;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
and polyadenylation of the 3' UTR.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515811; AAM74918.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
DB 10 HQGP 13

RESULT 36
Q8MH26 PRELIMINARY; PRT; 14 AA.
ID Q8MH26;
AC Q8MH26;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
contribute to increase the extraordinary diversity of DQA1 mRNA
isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533914; AAM94828.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
DB 10 HQGP 13

RESULT 37
Q8MH53 PRELIMINARY; PRT; 14 AA.
ID Q8MH53;
AC Q8MH53;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533914; AAM94828.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
DB 10 HQGP 13

RESULT 39
Q8MH27 PRELIMINARY; PRT; 14 AA.
ID Q8MH27;
AC Q8MH27;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;
RT "HLA-DQA1 genes generate multiple transcripts by alternative splicing
and polyadenylation of the 3' UTR.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF515810; AAM74917.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
DB 10 HQGP 13

RESULT 38
Q8MH20 PRELIMINARY; PRT; 14 AA.
ID Q8MH20;
AC Q8MH20;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE MHC class II antigen (Fragment).
GN HLA-DQA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
contribute to increase the extraordinary diversity of DQA1 mRNA
isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQA1 gene generates multiple transcripts by alternative splicing
and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533920; AAM94834.1; -.
FT NON TER 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYG 4
DB 10 HQGP 13

RESULT 39
Q8MH27 PRELIMINARY; PRT; 14 AA.
ID Q8MH27;
AC Q8MH27;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RP Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533913; AAM94827.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4
Db 10 HQGP 13

RESULT 40

Q8MH05
ID Q8MH05 PRELIMINARY; PRT; 14 AA.
AC Q8MH05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RP Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533935; AAM94849.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4
Db 10 HQGP 13

RESULT 41

Q8MH16
ID Q8MH16 PRELIMINARY; PRT; 14 AA.
AC Q8MH16;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RP Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533924; AAM94838.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4
Db 10 HQGP 13

RESULT 42

Q8MH38
ID Q8MH38 PRELIMINARY; PRT; 14 AA.
AC Q8MH38;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE MHC class II antigen (Fragment).
GN HLA-DQAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RP Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "A new splicing acceptor site and polyadenylation sequence signal
RT contribute to increase the extraordinary diversity of DQAI mRNA
RT isoforms.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;
RT "HLA DQAI gene generates multiple transcripts by alternative splicing
RT and polyadenylation of the 3' untranslated region.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF533902; AAM94816.1; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4

Db 10 HQGP 13

RESULT 43

Q8MH56 PRELIMINARY; PRT; 14 AA.

ID Q8MH56

AC Q8MH56; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQAI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M.M., Caillens H., Cadet F., Pabion M.;

RT "HLA-DQAI genes generate multiple transcripts by alternative splicing

RT and polyadenylation of the 3' UTR.";

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF515807; AAM74914.1; -.

FT NON_TER 1

SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;

Best Local Similarity 75.0%; Pred. No. 8.7e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4

Db 10 HQGP 13

RESULT 44

Q8MH14 PRELIMINARY; PRT; 14 AA.

ID Q8MH14

AC Q8MH14; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQAI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;

RT "A new splicing acceptor site and polyadenylation sequence signal

RT contribute to increase the extraordinary diversity of DQAI mRNA

RT isoforms.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;

RT "HLA DQAI gene generates multiple transcripts by alternative splicing

RT and polyadenylation of the 3' untranslated region.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF533926; AAM94840.1; -.

FT NON_TER 1

SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;

Best Local Similarity 75.0%; Pred. No. 8.7e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4

Db 10 HQGP 13

RESULT 45

Q8MH31 PRELIMINARY; PRT; 14 AA.

ID Q8MH31

AC Q8MH31; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE MHC class II antigen (Fragment).

GN HLA-DQAI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;

RT "A new splicing acceptor site and polyadenylation sequence signal

RT contribute to increase the extraordinary diversity of DQAI mRNA

RT isoforms.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Hoarau J.-J., Cesari M., Caillens H., Cadet F., Pabion M.;

RT "HLA DQAI gene generates multiple transcripts by alternative splicing

RT and polyadenylation of the 3' untranslated region.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF533909; AAM94823.1; -.

FT NON_TER 1

SQ SEQUENCE 14 AA; 1435 MW; C5EEA0FE15DF8EBD CRC64;

Query Match 34.5%; Score 20; DB 7; Length 14;

Best Local Similarity 75.0%; Pred. No. 8.7e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGP 4

Db 10 HQGP 13

Search completed: August 30, 2004, 10:55:26

Job time : 8.66554 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.55068 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGEGWVSM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	51.7	11	CA31_LITCI	P82089 litoria cit
2	29	50.0	11	CA32_LITCI	P82090 litoria cit
3	28	48.3	10	RPCH_PANBO	P08939 pandalus bo
4	28	48.3	10	HTF_NAUCI	P10939 nauphoeta c
5	26	44.8	10	GONL_SOUAC	P27429 squalus aca
6	25	43.1	8	AKH_WELML	P25423 melolontha
7	25	43.1	8	AKH_TABAT	P14595 tabanus atr
8	25	43.1	10	GON3_CHICK	P37043 gallus gall
9	25	43.1	10	GON3_ONCKE	P20367 oncorhynch
10	25	43.1	10	HTF_TABAT	P14596 tabanus atr
11	24	41.4	10	BRK_ONCMY	O9pr21 oncorhynch
12	23	40.5	12	RFL_CONSP	P58805 conus spuri
13	23	39.7	10	COXO_RAT	P80432 rattus norv
14	23	39.7	10	COXO_THUOB	P80982 thunnus obe
15	23	39.7	11	CORZ_PERAM	P11496 periplaneta
16	22	37.9	8	HTF1_PERAM	P04548 periplaneta
17	22	37.9	8	HTF_TENMO	P25419 tenebrio mo
18	22	37.9	13	BOML_PEGU	P42991 pseudophryn
19	21	36.2	10	GONI_PETMA	P04378 petromyzon
20	20	34.5	8	AKHG_GRYBI	P14086 gryllus bim
21	20	34.5	8	AKH_LIBAU	P25418 libellula a
22	20	34.5	10	HTF1_ROMMI	P18110 romalea mic
23	20	34.5	11	OAFI_SARBU	P83518 sarcophaga
24	20	34.5	12	NUDM_CANFA	P54713 canis famil
25	19	32.8	8	HTF2_PERAM	P04549 periplaneta
26	19	32.8	10	HTF2_CARMO	P11385 carausius m
27	19	32.8	10	HTF_HELZE	P16353 heliothis z
28	18	31.0	8	CKKN_MACEU	P30369 macropus eu
29	18	31.0	10	CAER_LITXA	P56264 litoria xan
30	18	31.0	10	GON3_PETMA	P30948 petromyzon
31	18	31.0	14	IF2G_RAT	P81795 rattus norv
32	18	31.0	14	MCRZ_METTM	P58816 methanobact
33	17	29.3	8	ALLI_CVDPO	P82152 cydia pomon

34	17	29.3	8	1	UF06_MOUSE	P38644 mus musculu
35	17	29.3	9	1	LMIP_LOCFI	P31799 locusta mig
36	17	29.3	10	1	BPP_VIPAS	P31351 vipera aspi
37	17	29.3	10	1	CA12_LITCI	P82086 litoria cit
38	17	29.3	11	1	RANC_RANPI	P08951 rana pipien
39	17	29.3	13	1	Bppl_BOTJA	P01020 bothrops ja
40	17	29.3	13	1	UP71_LITEW	P82050 litoria ewi
41	17	29.3	14	1	LPW_CITPR	P03056 citrobacter
42	17	29.3	14	1	LPW_ECOLI	P03053 escherichia
43	17	29.3	14	1	LPW_SALTY	P03054 salmonella
44	16	27.6	8	1	LCK2_LEUMA	P21141 leucophaea
45	16	27.6	9	1	BS43_SERPL	P83375 serratia pl

ALIGNMENTS

RESULT 1
CA31_LITCI
ID-CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA MEDLINE=20057701; PubMed=10589039;
RX Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue mountains tree frog Litoria citropa. Part 1. Sequence determination using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being sulfated.
CC -!- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family. InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;
Query Match 51.7%; Score 30; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 YGPGWV 7
|||
Db 4 YGTGWM 9
RESULT 2
CA32_LITCI
ID-CA32_LITCI STANDARD; PRT; 11 AA.
AC P82090;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.2/3.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montana tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry.";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502 (1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.24 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 FT MOD_RES 11 11 SULFATION.
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

 Query Match 50.0%; Score 29; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 27;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 YGPGW 6
 DB 4 YGTGW 8

 RESULT 3
 RPCH_PANBO STANDARD; PRT; 8 AA.
 AC P08939;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Red pigment concentrating hormone (RPCH).
 OS Pandanus borealis (Northern red shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
 OC Pandallidae; Pandalus.
 OX NCBI_TaxID=6703;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=75054965; PubMed=4433569;
 RA Fernlund P.;
 RT "Structure of the red-pigment-concentrating hormone of the shrimp,
 RT Pandanus borealis.";
 RL Biochim. Biophys. Acta 371:304-311 (1974).
 CC -!- FUNCTION: This hormone adapts the animal to light backgrounds by
 CC stimulating concentration of the pigment of its red body-
 CC chromatophores.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A61348; A61348.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Pigment; Hormone; Amidation; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 948 MW; 86786775B9C44736 CRC64;

 Query Match 48.3%; Score 28; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HYGPWG 6
 DB 3 NFSPGW 8

 RESULT 4
 HTF_NAUCI STANDARD; PRT; 10 AA.
 AC P10939;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosaemic hormone (HTH) (Hypertrehalosaemic neuropeptide).
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Leucophaea maderae (Madeira cockroach), and
 OS Blattella germanica (German cockroach).
 OS Gromphadorhina portentosa (Madagascan hissing cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Nauphoeta.
 OX NCBI_TaxID=6990, 6988, 6973, 36953;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=N.cinerea; TISSUE=Corpora cardiaca;
 RX MEDLINE=87100208; PubMed=3801028;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Amino acid sequence of a hypertrehalosaemic neuropeptide from the
 RT corpus cardiacum of the cockroach, Nauphoeta cinerea.";
 RL Biochem. Biophys. Res. Commun. 141:774-781 (1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.maderae, G.portentosa, and B.germanica;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=B.germanica;
 RX MEDLINE=91179584; PubMed=2080017;
 RA Veenstra J.A., Camps F.;
 RT "Structure of the hypertrehalosaemic neuropeptide of the German
 RT cockroach, Blattella germanica.";
 RL Neuropeptides 15:107-109 (1990).
 CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph of insects).
 CC major carbohydrate in the hemolymph of insects).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A26381; A26381.
 DR PIR; A60421; A60421.
 DR PIR; S08997; S08997.
 DR PIR; S08998; S08998.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1092 MW; 056236786775B9C4 CRC64;

 Query Match 48.3%; Score 28; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 36;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 HYGPWG 6
 DB 3 NFSPGW 8

RESULT 5

GOML_SQUAC STANDARD; PRT; 10 AA.

AC P27429;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin (Gonadotropin-releasing hormone) (GnRH) (LH-RH) (luliberin).
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OX NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92335300; PubMed=16311133;
 RA Lovejoy D.A., Fischer W.H., Ngamvongchon S., Craig A.G.,
 RA Nahorniak C.S., Peter R.E., Rivier J.E., Sherwood N.M.;
 RT "Distinct sequence of gonadotropin-releasing hormone (GnRH) in
 RT dogfish brain provides insight into GnRH evolution."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6373-6377(1992).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 DR PIR; A46030; A46030.
 DR InterPro; IPR002012; GnRH.
 DR Pfam; PF00446; GnRH; 1.
 DR PROSITE; PS00473; GnRH; 1.
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1204 MW; 284B32337871F5A3 CRC64;
 Query Match 44.8%; Score 26; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 80;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7
 : : :
 : : :
 DB 2 HWSHGWL 8

RESULT 6

AKH MELML STANDARD; PRT; 8 AA.

AC P25423;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH).
 OS Melolontha melolontha (Cockchafer), and
 OS Geotrupes stercorosus (Dor beetle), and
 OS Pachnoda marginata (Flower beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
 OC Scarabaeidae; Melolonthinae; Melolontha.
 OX NCBI_TaxID=7061, 7087, 7058;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M. melolontha, and G. stercorosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=91248100; PubMed=2039445;
 RA Gaede G.;
 RT "A unique charged tyrosine-containing member of the adipokinetic
 RT hormone/red-pigment-concentrating hormone peptide family isolated and
 RT sequenced from two beetle species."
 RL Biochem. J. 275:671-677(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P. marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;

RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
 RT "Primary structures of neuropeptides isolated from the corpora
 RT cardiaca of various cetonid beetle species determined by
 RT pulsed-liquid phase sequencing and tandem fast atom bombardment mass
 RT spectrometry."
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A58641; A58641.
 DR PIR; S15422; S15422.
 DR PIR; S21663; S21663.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1022 MW; 867AB775AB544736 CRC64;
 Query Match 43.1%; Score 25; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
 : : :
 : : :
 DB 3 NYSPDW 8

RESULT 7

AKH TABAT STANDARD; PRT; 8 AA.

AC P14595;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I) (DCC I).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera)."
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A33995; A33995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;
 Query Match 43.1%; Score 25; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
HTF_TABAT
ID HTF_TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosemic factor (HOTH) (Dipteran corpora cardiaca factor II) (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
CC -!- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
CC PIR; B33995; B33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
Db 4 FTGPGW 8

RESULT 11
BRK_ONCMY
ID BRK_ONCMY STANDARD; PRT; 10 AA.
AC Q9PRZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma.";
RL FEBS Lett. 334:75-78 (1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION, PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the bradykinin family.

DR PIR: S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 41.4%; Score 24; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGW 6
Db 4 PGW 6

RESULT 12
RFL_CONSP
ID RFL_CONSP STANDARD; PRT; 12 AA.
AC PS8805;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conorfamide-Srl.
OS Conus spurius (Alphabet cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=192919;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21605839; PubMed=11738233;
RA Maillo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
RA Olivera B.M., Heimer de la Coteria E.P.;
RT "Conorfamide, a Conus venom peptide belonging to the RFamide family of
RT neuropeptides.";
RL Toxicon 40:401-407 (2002).
CC -!- FUNCTION: Causes hyperactivity in mice.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neurotoxin; Toxin; Amidation.
FT MOD RES 12 12 AMIDATION
SQ SEQUENCE 12 AA; 1456 MW; 2510671E49D772D3 CRC64;

Query Match 40.5%; Score 23.5; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 GP-GWV 7
Db 1 GPMGWV 6

RESULT 13
COXO_RAT
ID COXO_RAT STANDARD; PRT; 10 AA.
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIc, mitochondrial (EC 1.9.3.1)
DE (VILIA) (Fragment).
GN COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;

RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";
 RL Eur. J. Biochem. 230:235-241(1995).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
 DR PIR; S65388; S65388.
 KW Oxidoreductase; Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;

Query Match 39.7%; Score 23; DB 1; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 HY--GPG 5
 |||||
 Db 2 HYEGPG 8

RESULT 14

COCO THUOB
 ID -COCO THUOB STANDARD; PRT; 10 AA.
 AC P80982;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei; Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Heart, and Liver;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F., Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
 CC -!- SIMILARITY: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIIC family.
 DR PIR; S77990; S77990.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match 39.7%; Score 23; DB 1; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 HY--GPG 5
 |||||
 Db 2 HYEGPG 8

RESULT 15

CORZ PERAM
 ID CORZ PERAM STANDARD; PRT; 11 AA.
 AC P11496;
 DT 01-OCT-1989 (Rel. 12, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 39.7%; Score 23; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 2.9e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
 |||||
 Db 5 YSRGWTN 11

RESULT 16

HTFL PERAM
 ID HTFL PERAM STANDARD; PRT; 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosaemic factor I (Neuropeptide M-I) (Periplaneta CC-I) (PEA-CAH-I) (Ied-CC-I) (Hypertrehalosaemic neuropeptide I).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E., Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.

RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kallish F., Kramer S.J., McEnroe G.A., Miller C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with cardioacceleratory and hyperglycemic activity from the corpora cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;

GAEDE G., KELLNER R.;
 "The metabolic neuropeptides of the corpus cardiacum from the potato beetle and the American cockroach are identical.";
 Peptides 10:1287-1289 (1989).
 [4]
 RN
 RP
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae, Gromphadorhina portentosa, Blattella germanica and Blatta orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
 CC
 CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph of insects.
 CC the major carbohydrate in the hemolymph of insects.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A05169; A05169.
 DR PIR; A44960; A44960.
 DR PIR; A49823; A49823.
 DR PIR; S08995; S08995.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 37.9%; Score 22; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPGW 6
 Db 3 NFSPNW 8
 RESULT 17
 HTF TENMO STANDARD; PRT; 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosaemic factor (HOTH) (Hypertrehalosaemic neuropeptide).
 OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7075;
 RN [1]
 RP
 RC SPECIES=T.molitor, and Z.rugipes;
 RX TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Kosinski G.;
 RT "The primary structure of the hypertrehalosaemic neuropeptide from tenebrionid beetles: a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459 (1990).
 CC
 CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that elevate the level of trehalose in the hemolymph of insects.
 CC the major carbohydrate in the hemolymph of insects.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A43976; A43976.
 DR PIR; B43976; B43976.
 DR InterPro; IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 DR Neuropeptide; Amidation; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 37.9%; Score 22; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
 Db 3 NFSPNW 8

RESULT 18

BOML_PSEGU STANDARD; PRT; 13 AA.
 AC P42991;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Bombesin-like peptide L (PG-L).

OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.

OX NCBI_TaxID=30349;
 RN [1]

SEQUENCE.

RP
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;

RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;

RT "Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog Pseudophryne guntheri.";

RL Peptides 11:299-304 (1990).
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin family.

CC PIR; A60409; A60409.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation;

KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;

Query Match 37.9%; Score 22; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 5.1e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
 Db 4 GPQW 7

RESULT 19

GONL_PETWA STANDARD; PRT; 10 AA.

ID GONL_PETWA
 AC P04378;

DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)

DE (Luliberin I).
 OS Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.

OX NCBI_TaxID=7757;
 RN [1]

SEQUENCE.

RC TISSUE=Brain;
RX MEDLINE=86168192; PubMed=3514603;
RA Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;
RT "Primary structure of gonadotropin-releasing hormone from lamprey
brain.";
RL J. Biol. Chem. 261:4812-4819(1986).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A01412; RHLGMS.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 36.2%; Score 21; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.8e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HYGPW 6
|||
Db 2 HYSLEW 7

RESULT 20
AKHG GRYBI STANDARD; PRT; 8 AA.
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (Two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]
RP SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=8610653; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
of a peptide with adipokinetic activity from the corpora cardiaca of
the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
diglycerides from the fat body and then stimulates the flight
muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPW 6
:|||
Db 3 NFSTGW 8

RESULT 21
AKH LIBAU STANDARD; PRT; 8 AA.
AC P25418;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH).
OS Libellula auripennis (Skimmer dragonfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX NCBI_TaxID=6966;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90359055; PubMed=2390213;
RA Gaede G.;
RT "The putative ancestral peptide of the adipokinetic/red-pigment-
concentrating hormone family isolated and sequenced from a
dragonfly.";
RL Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC -!- FUNCTION: This hormone, released from cells in the corpora
cardiaca after the beginning of flight, causes release of
diglycerides from the fat body and then stimulates the flight
muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; S10596; S10596.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 978 MW; 8665A771A9C452D6 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPW 6
:|||
Db 3 NFSTGW 8

RESULT 22
HTFL ROMMI STANDARD; PRT; 10 AA.
AC P18110;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RO I (Hypertrehalosaemic factor).
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Romaleidae; Romalea.
OX NCBI_TaxID=7007;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from

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RT the lubber grasshopper, Romalea microptera."
RL Peptides 9:681-688(1998).
CC -!- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC DR InterPro: IPR002047; AKH.
CC DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1163 MW; 056236745771A9C4 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 8.6e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
Db 3 NPTFNW 8

RESULT 23
OAIIF_SARBU STANDARD; PRT; 11 AA.
AC P835I8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE OAIIF(1-9); Neb-OAIIF(1-7)].
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Ovary;
RX MEDLINE=22272747; PubMed=12383874;
RA Vandingenen A., Hens K., Badgerman G., Macours N., Schoofs L.,
RA De Loof A., Huybrechts R.;
RT "Isolation and characterization of an angiotensin converting enzyme
RT substrate from vitellogenic ovaries of Neobellieria bullata."
RL Peptides 23:1853-1863(2002).
CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
CC vitro.
CC -!- PTM: ACE hydrolyzes Neb-OAIIF by sequentially cleaving off two C-
CC terminal dipeptides.
CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
FT PEPTIDE 1 11 NEB-OAIIF.
FT PEPTIDE 1 9 NEB-OAIIF(1-9).
FT PEPTIDE 1 7 NEB-OAIIF(1-7).
SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 WVSM 9
Db 8 WISL 11

RESULT 24
NUDM CANFA STANDARD; PRT; 12 AA.
AC P547I3;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE NADH-ubiquinone oxidoreductase 42 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Complex I-42KD) (CI-42KD) (Fragment).
GN NDUFA10.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- FUNCTION: Transfer of electrons from NADH to the respiratory
CC chain. The immediate electron acceptor for the enzyme is believed
CC to be ubiquinone.
CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC -!- COFACTOR: Binds 1 FAD per subunit.
CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC This a component of the hydrophobic protein fraction.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
DR HSC-2DPAGE; P547I3; DOG.
KW Oxidoreductase; NAD; Ubiquinone; Flavoprotein; FAD; Mitochondrion.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1284 MW; 3CCD4E2B36EDD737 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YGP 4
Db 3 YGP 5

RESULT 25
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P045I9;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrahalosemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (PeA-CAH-II) (LeD-CC-II) (Hypertrahalosemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffter M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).

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[3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Rinehart R.;
 RT "The metabolic neuropeptides of the corpus cardiacum from the potato
 beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289 (1989).
 [4]
 RP SEQUENCE.
 RC SPECIES=S.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
 the corpora cardiaca of the cockroaches *Leucophaea maderae*,
Gromphadorhina portentosa, *Blattella germanica* and *Blatta orientalis*
 and of the stick insect *Extatosoma tiaratum* assigned by tandem fast
 atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354 (1990).
 CC -1- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
 elevate the level of trehalose in the hemolymph of insects).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; B44960; B4960.
 DR PIR; B49823; B49823.
 DR PIR; S08996; S08996.
 DR InterPro; IPR02047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;
 Query Match 32.8%; Score 19; DB 1; Length 8;
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps
 QY 2 YGPGW 6 : : :
 DB 4 FTFNW 8 : : :
 RESULT 26
 HTF2 CARMO
 ID HTF2 CARMO STANDARD; PRT; 10 AA.
 AC P11355;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
 neuropeptide II).
 DE Carausius morosus (Indian stick insect), and
 OS Extatosoma tiaratum (Stick insect).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;
 OC Heteronemiidae; Carausius.
 OX NCBI_TaxID=7022, 7024;
 [1]
 RP SEQUENCE.
 RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
 RX MEDLINE=87157103; PubMed=3828078;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structure of the hypertrehalosaemic factor II from the
 corpus cardiacum of the Indian stick insect, *Carausius morosus*,
 determined by fast atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 368:67-75 (1987).
 [2]
 RP SEQUENCE.
 RC SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosaemic neuropeptides isolated from

the corpora cardiaca of the cockroaches *Leucophaea maderae*,
RT *Gromphadorfina portentosa*, *Blattella germanica* and *Blatta orientalis*
RT and of the stick insect *Extatosoma tlatum* assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL *Biol. Chem. Hoppe-Seyler* 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RC SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiacum.";
RL *Biochem. Biophys. Res. Commun.* 189:1303-1309(1992).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR: JCI416; JCI416.
DR PIR: S09138; S09138.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Glycoprotein; Pyrrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).
FT MOD RES 10 10 AMIDATION.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;

Query Match 32.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps

Qy 2 YGPGW 6
 : | |
Db 4 FTENW 8

RESULT 27
HTF_HELZE
ID _HTF_HELZE STANDARD; PRT; 10 AA.
AC PI6353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic hormone (Hez-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helioverpa.
OX NCBI_Taxid=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=98326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
RA Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuropeptide hormone from
RT Heliothis zea with hypertrehalosaemic and adipokinetic activities.";
RL *Biochem. Biophys. Res. Commun.* 155:344-350(1988).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR: A31571; A31571.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 32.8%; Score 19; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6
: ||
Db 4 FSSGW 8

RESULT 28
CCKN_MACEU STANDARD; PRT; 8 AA.
AC P30369;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.

OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]

RP SEQUENCE.
RC SPECIES=M.eugenii, and D.viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian marsupials";
RL Peptides 9:429-431(1988).
CC -!- FUNCTION: This peptide hormone induces gall bladder contraction and the release of pancreatic enzymes in the gut. Its function in the brain is not clear.

CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR PIR; A43001; A43001.
DR PIR; P00012; P00012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2 2 SULFATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 31.0%; Score 18; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GWV 7
: ||
Db 4 GWM 6

RESULT 29
CAER_LITXA STANDARD; PRT; 10 AA.
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein.

OS Litoria xanthera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=79697;
RN [1]

RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
Ramsay S.L.;

RT "New caerin antibacterial peptides from the skin glands of the Australian tree frog Litoria xanthera.";
RL J. Pept. Sci. 3:181-185(1997).
CC -!- FUNCTION: Hypotensive neuropeptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1230 MW; 99DBF3837861BB5A CRC64;

Query Match 31.0%; Score 18; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GWV 7
: ||
Db 6 GWM 8

RESULT 30
GON3_PETMA STANDARD; PRT; 10 AA.
AC P30948;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (luliberin III).
DE Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]

RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93178316; PubMed=8440174;
RA Sower S.A., Chiang Y.-C., Lovas S., Conlon J.M.;
RT "Primary structure and biological activity of a third gonadotropin-releasing hormone from lamprey brain.";
RL Endocrinology 132:1125-1131(1993).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the GnRH family.

DR InterPro; IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1277 MW; 284B36237AA1F5A3 CRC64;

Query Match 31.0%; Score 18; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HVGPGW 6
: ||
Db 2 HWSHDW 7

RESULT 31
IF2G_RAT STANDARD; PRT; 14 AA.
ID IF2G_RAT
AC P81795;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic
DE translation initiation factor 2 gamma subunit) (eIF-2-gamma) (PP42)
DE (Fragment).
DE EIP2S3 OR EIP2G.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96374441; PubMed=8780732;
RA Gil C., Plana M., Riera M., Icarle E.;
RT "Rat liver pp49, a protein that forms complexes with protein kinase
RT CK2, is composed of the beta and the gamma subunits of translation
RT initiation factor eIF-2.";
RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
CC -!- FUNCTION: eIF-2 functions in the early steps of protein synthesis
CC by forming a ternary complex with GTP and initiator tRNA. This
CC complex binds to a 40S ribosomal subunit, followed by mRNA binding
CC to form a 43S preinitiation complex. Junction of the 60S ribosomal
CC subunit to form the 80S initiation complex is preceded by
CC hydrolysis of the GTP bound to eIF-2 and release of an eIF-2-GDP
CC binary complex. In order for eIF-2 to recycle and catalyze another
CC round of initiation, the GDP bound to eIF-2 must exchange with GTP
CC by way of a reaction catalyzed by eIF-2b.
CC -!- SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
CC chain.
CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC EIF2G subfamily.
KW Initiation factor; Protein biosynthesis; GTP-binding.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1511 MW; D86EDA955ABEFA12 CRC64;

Query Match 31.0%; Score 18; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PGVWS 8
|||
Db 9 PGVWS 13

RESULT 32
MCRZ METTM STANDARD; PRT; 14 AA.
AC P58816;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
DE gamma) (Fragment).
GN MRCG.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]
RP SEQUENCE.
RX MEDLINE=91099370; PubMed=2269306;
RA Robert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in
RT Methanobacterium thermoautotrophicum strain Marburg and Delta H.";
RL Eur. J. Biochem. 194:871-877(1990).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
CC to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.

CC Coenzyme F430 is a yellow nickel porphyrinoid.
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains.
CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CC CONTAINS MOSTLY MCR I.
DR PIR; E69017; E69017.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT INIT_MET 0
FT NON_TER 14
SQ SEQUENCE 14 AA; 1557 MW; 97E9439C4223B871 CRC64;

Query Match 31.0%; Score 18; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGPG 5
|||
Db 6 YTPG 9

RESULT 33
ALLI CYDPO STANDARD; PRT; 8 AA.
ID ALLI_CYPDO
AC P82152;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin I.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 934 MW; C82879C45B51F775 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYPG 5
|||
Db 3 HYNFG 7

RESULT 34
UF06 MOUSE STANDARD; PRT; 8 AA.
ID UF06_MOUSE
AC P38644;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009507; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

RT "Separation and sequencing of familiar and novel murine proteins
RT using preparative two-dimensional gel electrophoresis."
RL Electrophoresis 15:735-745 (1994).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
FT protein is: 5.2, its MW is: 50 kDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPG 5
DB 1 HSEPG 5

RESULT 35

LMIP LOCMI STANDARD; PRT; 9 AA.
AC P31759;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locustamyo-inhibiting peptide (LOW-MIP).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.

RX MEDLINE=92179466; PubMed=1796179;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
"Isolation, identification and synthesis of locustamyo-inhibiting
RT peptide (LOW-MIP), a novel biologically active neuropeptide from
RT Locusta migratoria."
RL Regul. Pept. 36:111-119 (1991).
CC -1- FUNCTION: Suppresses spontaneous contractions of the hindgut and
CC oviduct.

CC -1- TISSUE SPECIFICITY: Neurons located in two ventral cell clusters
CC in the subesophageal ganglion.

DR PIR; A60065; AKLOIM.
KW Amidation; Neuropeptide.
FT MOD_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
DB 8 GW 9

RESULT 36

BPP VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Viperas aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Viperas.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.

Query Match 29.3%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Viperas aspis aspis."
RL Int. J. Biochem. 22:767-771 (1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A60377; XASNPC.
DR KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
DB 2 GW 3

RESULT 37

CA12 LITCI STANDARD; PRT; 10 AA.
ID CA12_LITCI
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2V4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770, 30345;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2 AND 1.2V4).
RC SPECIES=L.citropa; TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502 (1999).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L.splendida; TISSUE=Skin secretion;
RX MEDLINE=20069371; PubMed=10601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
RT tree frog Litoria splendida. The discovery of the aquatic male sex
RT pheromone splendipherin, together with Phe8 caerulein and the
RT antibiotic peptide caerin 1.10."
RL Eur. J. Biochem. 267:269-275 (2000).
CC -1- FUNCTION: Hypotensive neuropeptide (Probable).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 1.2V4 differs from isoform 1.2 in not being
CC sulfated.

CC -1- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;

Best Local Similarity 100.0%; Pred. No. 2.8e+03; Indels 0; Gaps 0;
Matches 2; Conservative 0; Mismatches 0;

Qy 5 GW 6
Db 6 GW 7

RESULT 38

RP RANC RANPI STANDARD; PRT; 11 AA.
AC P08951;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatensin-C.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;

RA Nakajima T.;

RL Unpublished results, cited by:

RP Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;

RL Comp. Biochem. Physiol. 77C:93-108(1984).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin family.

DR InterPro; IPR000874; Bombesin.

DR Pfam; PF02044; Bombesin; 1.

DR PROSITE; PS00257; BOMBESIN; 1.

KW Amphibian defense peptide; Bombesin family; Amidation.

FT MOD RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 11;

Best Local Similarity 40.0%; Pred. No. 3.1e+03; Indels 0; Gaps 0;
Matches 2; Conservative 1; Mismatches 2;

Qy 4 PGWVS 8

Db 3 PQWAT 7

RESULT 39

ID BPPI BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13A) (Angiotensin-converting enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724, 8723;
RN [1]

RP SEQUENCE.

RC SPECIES=B.jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;

RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,

RA Kocy O.;

RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops

jararaca. Isolation, elucidation of structure, and synthesis.";

RL Biochemistry 10:4033-4039(1971).

RN [2]

RP SEQUENCE.

RC SPECIES=B.insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;

RA Cintra A.C.O., Vieira C.A., Giglio J.R.;

RT "Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.";

RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it. It acts as an indirect hypotensive agent.

DR PIR; A01253; XAVI9B.

KW Hypotensive agent; Pyrrolidone carboxylic acid.

FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.6e+03; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0;

Qy 5 GW 6

Db 3 GW 4

RESULT 40

UP71 LITEW

ID UP71 LITEW STANDARD; PRT; 13 AA.

AC P82050;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Uperin 7.1 [Contains: Uperin 7.1.1].

OS Litoria ewingi (Brown tree frog) (Ewing's tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI_TaxID=104896;

RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RA Steinborner S.T., Bowie J.H., Tyler M.J., Wallace J.C.;

RT "An unusual combination of peptides from the skin glands of Ewing's tree frog, Litoria ewingi. Sequence determination and antimicrobial activity.";

RT Aust. J. Chem. 50:889-894(1997).

CC -!- FUNCTION: Uperin 7.1 shows antibacterial activity against L.lactis and S.suberis. Uperin 7.1.1 is inactive.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

CC -!- MASS SPECTROMETRY: MW=1427; METHOD=FAB; RANGE=1-13.

CC -!- MASS SPECTROMETRY: MW=1184; METHOD=FAB; RANGE=3-13.

KW Amphibian defense peptide; Antibiotic; Amidation.

FT PEPTIDE 1 13 UPERIN 7.1.

FT PEPTIDE 3 13 UPERIN 7.1.1.

FT MOD RES 13 13 AMIDATION.

SQ SEQUENCE 13 AA; 1429 MW; DE17C7204CCAE322 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.6e+03; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0;

Qy 5 GW 6

Db 1 GW 2

RESULT 41

LPW CITFR

ID LPW CITFR STANDARD; PRT; 14 AA.

AC P03056;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Trp operon leader peptide.
GN TRPL
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83007061; PubMed=6749821;
RA Blumenberg M., Yanofsky C.;
RA "Evolutionary divergence of the Citrobacter freundii tryptophan
RT operon regulatory region: comparison with other enteric bacteria.";
J. Bacteriol. 152:57-62(1982).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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CC -----
CC EMBL; J01557; -; NOT_ANNOTATED_CDS.
DR PIR; A03592; LFEBC.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 14 AA; 1720 MW; 5B792A473B8048E7 CRC64;
Query Match 29.3%; Score 17; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GW 6
Db 9 GW 10
RESULT 42
ID LPW_ECOLI STANDARD; PRT; 14 AA.
AC P03053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR TRPEE OR B1265 OR C5494 OR Z2545 OR ECS1837 OR SF1268 OR
GN S4805.
OS Escherichia coli,
OS Escherichia coli O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=82150258; PubMed=7038627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RA Horowitz H., van Cleemput M., Wu A.M.;
RT "The complete nucleotide sequence of the tryptophan operon of
RT Escherichia coli";
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA Yanofsky C.;
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT Escherichia coli";

J. Mol. Biol. 103:351-381(1976).
[3]
RN SEQUENCE FROM N.A.
RP SPECIES=E.coli;
RC MEDLINE=80101455; PubMed=118451;
RX Oxender D.L., Zurawski G., Yanofsky C.;
RA "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RT secondary structure involving the tryptophan codon region.";
Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12";
DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157";
Nucleic Acids Res. 30:4432-4441(2002).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;

```

RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786 (2003).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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CC -----
DR EMBL; J01714; AAA57296.1; -.
DR EMBL; A04494; CAA00361.1; -.
DR EMBL; AE000224; AAC74347.1; -.
DR EMBL; AE016760; AAN80196.1; -.
DR EMBL; AE005380; AAG56550.1; -.
DR EMBL; AP002556; BAB35260.1; -.
DR EMBL; AE015153; AAN42881.1; -.
DR EMBL; AE016982; AAP16766.1; -.
DR PIR; A03589; LFECW.
DR PIR; B85761; B85761.
DR PIR; E90858; E90858.
DR EcoGene; EG11274; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1723 MW; 5B793063E804A37 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
DB 9 GW 10

RESULT 43
LPW SALTY STANDARD; PRT; 14 AA.
ID LPW SALTY STANDARD; PRT; 14 AA.
AC P03054;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trp operon leader peptide.
GN TRP OR TRPEE OR STM1722.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=78196931; PubMed=3511195;
RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
RT regions of the tryptophan operons of Escherichia coli and Salmonella
RT typhimurium.";
RL J. Mol. Biol. 121:193-217 (1978).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856 (2001).
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CC -----
DR EMBL; M24960; -. NOT ANNOTATED_CDS.
DR EMBL; AE008776; AAL20640.1; -.
DR PIR; A03590; LFEBWT.
DR StyGene; SG10400; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1635 MW; 49F2A47362248E7 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GW 6
DB 9 GW 10

RESULT 44
LCK2 LEUMA STANDARD; PRT; 8 AA.
ID LCK2 LEUMA STANDARD; PRT; 8 AA.
AC P21141;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Leucokinin II (I-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of two neuropeptides
RT from Leucophaea maderae: members of a new family of
RT Cephalomyotropins.";
RL Comp. Biochem. Physiol. 84C:205-211 (1986).
CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
CC activity of cockroach proctodeum (hindgut).
CC -!- SUBCELLULAR LOCATION: Secreted.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;

Query Match 27.6%; Score 16; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PGWVS 8
DB 2 PGFSS 6

RESULT 45
BS43 SERPL STANDARD; PRT; 9 AA.
ID BS43 SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.

```

OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against *Erwinia amylovora*, the fire blight pathogen.";
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC *E. amylovora*.
KW Antibiotic; Bacteriocin.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1E66D412C871E1FB CRC64;

Query Match 27.6%; Score 16; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYG 3
Db 3 HHG 5

Search completed: August 30, 2004, 10:50:23
Job time : 1.55068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-8

Perfect score: 58

Sequence: 1 HVGPGWVSM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	48.3	8	A61348	red pigment-concen
2	28	48.3	10	A60421	hypertrrehalosemic
3	28	48.3	10	S08997	hypertrrehalosemic
4	28	48.3	10	S08998	hypertrrehalosemic
5	28	48.3	10	A26381	hypertrrehalosemic
6	26	44.8	8	S55310	adipokinetic hormo
7	26	44.8	8	A58620	adipokinetic hormo
8	26	44.8	9	PT0231	Ig heavy chain CDR
9	26	44.8	10	A46030	gonadoliberin I -
10	25	43.1	8	S15422	adipokinetic hormo
11	25	43.1	8	A33995	adipokinetic hormo
12	25	43.1	8	A58641	adipokinetic hormo
13	25	43.1	8	S21663	neuropeptide - flo
14	25	43.1	10	RHAQ2	gonadoliberin II -
15	25	43.1	10	A61126	gonadoliberin II -
16	25	43.1	10	B46030	gonadoliberin II -
17	25	43.1	10	B33995	gonadoliberin II -
18	25	43.1	10	A21114	gonadoliberin II -
19	25	43.1	14	S33802	chaperone, TCPI-re
20	24	41.4	10	S39030	lysyl-bradykinin -
21	24	41.4	11	S70338	napin small chain
22	24	41.4	14	PH1322	Ig heavy chain DJ
23	23	39.7	9	PT0288	Ig heavy chain CDR
24	23	39.7	10	S65388	cytochrome-c oxida
25	23	39.7	10	S77990	cytochrome-c oxida
26	23	39.7	10	PT0289	Ig heavy chain CDR
27	23	39.7	11	S05002	corazonin - Americ
28	23	39.7	11	PT0302	Ig heavy chain CDR
29	22	37.9	8	S08995	hypertrrehalosemic

ALIGNMENTS

RESULT 1

A61348 red pigment-concentrating hormone - northern shrimp

N;Alternate names: blanching hormone

C;Species: Pandanus borealis (northern shrimp)

C;Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C;Accession: A61348; S07139

R;Fennlund, P.; Josefsson, L.

Science 177, 173-175, 1972

A;Title: Crustacean color-change hormones: amino acid sequence and chemical synthesis.

A;Reference number: A61348; MUID:7228738; PMID:5041363

A;Accession: A61348

A;Molecule type: protein

A;Residues: 1-8 <PER1>

R;Fennlund, P.

Biochim. Biophys. Acta 371, 304-311, 1974

A;Title: Structure of the red-pigment-concentrating hormone of the shrimp, Pandanus borealis

A;Reference number: S07139; MUID:75054965; PMID:4433569

A;Accession: S07139

A;Molecule type: protein

A;Residues: 'E', 2-8 <PER2>

A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C;Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-

zed pigment-containing cells.

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HVGPGW 6

::: |||

Db 3 NFSPGW 8

RESULT 2

A60421 hypertrrehalosemic hormone - German cockroach

N;Alternate names: Bld-HrTH

C;Species: Blattella germanica (German cockroach)

C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 31-Oct-1997

C;Accession: A60421; S09137

R;Veenstra, J.A.; Camps, F.

Neuropeptides 15, 107-109, 1990

A;Title: Structure of the hypertrrehalosemic neuropeptide of the German cockroach, Blattella

A;Reference number: A60421; MUID:91179584; PMID:2080017

A;Accession: A60421

A;Molecule type: protein

A;Residues: 1-10 <VEE>

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30      22      37.9      8      2      A49823      adipokinetic hormo
31      22      37.9      8      2      A44960      neuropeptide Lec-C
32      22      37.9      8      2      A43976      hypertrrehalosemic
33      22      37.9      8      2      B43976      hypertrrehalosemic
34      22      37.9      8      2      A05169      neuropeptide M-I -
35      22      37.9      8      2      S53789      neuropeptide Pec-H
36      22      37.9      10     2      S53789      bombesin-like pept
37      22      37.9      13     2      A60409      gonadoliberin - se
38      21      36.2      10     1      RHLMGS      spermadhesin AQW-3
39      21      36.2      11     2      S68649      gonadoliberin - se
40      21      36.2      11     2      PT0209      T-cell receptor al
41      21      36.2      12     2      PT0274      Ig heavy chain CDR
42      21      36.2      14     2      S03530      Ig heavy chain J r
43      20      34.5      8      2      A28004      adipokinetic hormo
44      20      34.5      8      2      S10596      adipokinetic hormo
45      20      34.5      8      2      S11545      adipokinetic hormo

```

R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry

A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
::|||
Db 3 NFSPGW 8

RESULT 3

hypertrehalosemic neuropeptide Bld-HrTH - cockroach (Gromphadorina portentosa)
C;Species: Gromphadorina portentosa
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08997

R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry

A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08997
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
::|||
Db 3 NFSPGW 8

RESULT 4

hypertrehalosemic neuropeptide Bld-HrTH - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 30-Jun-1992 #sequence_revision 14-Sep-1994 #text_change 24-Oct-1997
C;Accession: S08998

R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry

A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08998
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
::|||
Db 3 NFSPGW 8

RESULT 5

hypertrehalosemic hormone - gray cockroach
C;Species: Nauphoeta cinerea (gray cockroach)
C;Date: 31-Mar-1998 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: A26381

R;Gaede, G.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 141, 774-781, 1986
A;Title: Amino acid sequence of a hypertrehalosaemic neuropeptide from the corpora entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry

A;Reference number: A26381; MUID:87100208; PMID:3801028
A;Accession: A26381
A;Molecule type: protein
A;Residues: 1-10 <GAD>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have used the sequence of the mature peptide
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
::|||
Db 3 NFSPGW 8

RESULT 6

adipokinetic hormone - damselfly (Pseudagrion inconspicuum)
N;Alternate names: Psi-AKH
C;Species: Pseudagrion inconspicuum
C;Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: S55310

R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum and Zygoptera
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: S55310
A;Molecule type: protein
A;Residues: 1-8 <JAN>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 44.8%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
::|||
Db 3 NFSPGW 8

RESULT 7

adipokinetic hormone - damselfly (Ischnura senegalensis)
C;Species: Ischnura senegalensis
C;Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-May-1999
C;Accession: A58620
R;Janssens, M.P.E.; Kellner, R.; Gaede, G.
Biochem. J. 302, 539-543, 1994
A;Title: A novel adipokinetic octapeptide found in the damselflies Pseudagrion inconspicuum and Zygoptera
A;Reference number: S55310; MUID:94379987; PMID:8093008
A;Accession: A58620
A;Molecule type: protein

Query Match 44.8%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HYGPGW 6
::|||
Db 3 NFSPGW 8

A:Residues: 1-8 <JAN>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 44.8%; Score 26; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPWG 6

DB 3 NPTPGW 8

RESULT 8

PT0231

Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0231

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0231

A:Molecule type: DNA

A:Residues: 1-9 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 44.8%; Score 26; DB 2; Length 9;

Best Local Similarity 57.1%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGWVS 8

DB 3 HSSGWVS 9

RESULT 9

A46030

Gonadoliberin I - spiny dogfish

N:Alternate names: gonadotropin-releasing hormone

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Dec-1998

C:Accession: A46030

R:Lovejoy, D.A.; Fischer, W.H.; Nganvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A:Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain pro

A:Reference number: A46030; MUID:92335300; PMID:1631133

A:Accession: A46030

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <LOV>

C:Keywords: hormone; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 44.8%; Score 26; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 1.5e+02;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPWGV 7

DB 2 HWSHGWL 8

RESULT 10

S15422

adipokinetic hormone - cockchafer

C:Species: Melolontha melolontha (cockchafer)

C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997

C:Accession: S15422

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A:Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pig

A:Reference number: S15422; MUID:91248100; PMID:2039445

A:Accession: S15422

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 43.1%; Score 25; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPWG 6

DB 3 NYSPDW 8

RESULT 11

A33995

adipokinetic hormone - black horse fly

C:Species: Tabanus atratus (black horse fly)

C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997

C:Accession: A33995

R:Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Y.

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A:Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehalc

A:Reference number: A33995; MUID:90046758; PMID:2813385

A:Accession: A33995

A:Molecule type: protein

A:Residues: 1-8 <JAP>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F:8/Modified site: amidated carboxyl end (Trp) #status predicted

Query Match 43.1%; Score 25; DB 2; Length 8;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6

DB 4 FTPGW 8

RESULT 12

A58641

adipokinetic hormone - dor beetle

C:Species: Geotrupes stercorosus (dor beetle)

C:Date: 28-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997

C:Accession: A58641

R:Gaede, G.

Biochem. J. 275, 671-677, 1991

A:Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red-pig

A:Reference number: S15422; MUID:91248100; PMID:2039445

A:Accession: A58641

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 43.1%; Score 25; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPWG 6

DB 3 NYSPDW 8

RESULT 13
S21663
neuropeptide - flower beetle (Pachnoda marginata)
C;Species: Pachnoda marginata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S21663
R;Gaede, G.; Lopata, A.; Kallner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of various ectometry.
A;Reference number: S21663; MUID:92265187; PMID:1586453
A;Accession: S21663
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <GAE>

Query Match 43.1%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPWG 6
: |||
Db 3 NYSDDW 8

RESULT 14
RHAQ2
gonadoliberin II - American alligator
N;Alternate names: gonadotropin-releasing hormone II
C;Species: Alligator mississippiensis (American alligator)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: B60066
R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of alligators.
A;Reference number: A60066; MUID:91352338; PMID:1882082
A;Accession: B60066
A;Molecule type: protein
A;Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1/Modified site: pyroglutamic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPWG 6
: |||
Db 2 HWSHGW 7

RESULT 15
A61126
gonadoliberin - spotted ratfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Hydrolagus colliei (spotted ratfish)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 18-Mar-1997
C;Accession: A61126
R;Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T. Gen. Comp. Endocrinol. 82, 152-161, 1991
A;Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocope
A;Reference number: A61126; MUID:91340067; PMID:1678723
A;Accession: A61126
A;Molecule type: protein
A;Residues: 1-10 <LOV>
A;Experimental source: brain
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
F;1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 43.1%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPWG 6
: |||
Db 2 HWSHGW 7

RESULT 16
B46030
gonadoliberin II - spiny dogfish
N;Alternate names: gonadotropin-releasing hormone
C;Species: Squalus acanthias (spiny dogfish)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jan-2003
C;Accession: B46030
R;Lovejoy, D.A.; Fischer, W.H.; Ngamvongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R. Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992
A;Title: Distinct sequence of gonadotropin-releasing hormone (GnRH) in dogfish brain protein.
A;Reference number: A46030; MUID:92335300; PMID:1631133
A;Accession: B46030
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <LOW>
C;Superfamily: gonadoliberin
C;Keywords: hormone; pyroglutamic acid
F;1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 43.1%; Score 25; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPWG 6
: |||
Db 2 HWSHGW 7

RESULT 17
B33995
hypotrehalosemic hormone - black horse fly
C;Species: Tabanus atratus (black horse fly)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 31-Oct-1997
C;Accession: B33995
R;Taffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang, Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989
A;Title: Primary structure of two neuropeptide hormones with adipokinetic and hypotrehal
A;Reference number: A33995; MUID:90046758; PMID:2813385
A;Accession: B33995
A;Molecule type: protein
A;Residues: 1-10 <JAF>
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyroglutamic acid (Gln) #status predicted
F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match 43.1%; Score 25; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGPWG 6
: |||
Db 4 FTGPWG 8

RESULT 18
A21114
gonadoliberin - chum salmon
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
C;Accession: A21114
R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983

A;Title: Characterization of a teleost gonadotropin-releasing hormone.
A;Reference number: A21114; MUID:83195140; PMID:6341999

A;Accession: A21114

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SHE>

Query Match 43.1%; Score 25; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7
|: ||:
Db 2 HWSYGWL 8

RESULT 19

S33802

C;Species: TCPI-related - oat

C;Species: Avena sativa (oat)

C;Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999

C;Accession: S33802

R;Mummert, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaefer

Nature 363, 644-648, 1993

A;Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its photo

A;Reference number: S33800; MUID:93288140; PMID:8099715

A;Accession: S33802

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-14 <MUM>

Query Match 43.1%; Score 25; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWV 7
||: |:
Db 8 GPWVI 12

RESULT 20

S39030

C;Species: lysyl-bradykinin - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 18-Aug-2000

C;Accession: S39030

R;Conlon, J.M.; Olson, K.R.

FEBS Lett. 334, 75-78, 1993

A;Title: Purification of a vasoactive peptide related to lysyl-bradykinin from trout pla

A;Reference number: S39030; MUID:94039817; PMID:8224232

A;Accession: S39030

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CON>

C;Superfamily: unassigned animal peptides

Query Match 41.4%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PCW 6
|||:
Db 4 PCW 6

RESULT 21

S70338

C;Species: napin small chain S3A - Swedish turnip (fragment)

C;Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)

C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

A;Accession: S70338

R;Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.

Biochim. Biophys. Acta 1295, 23-33, 1996

A;Title: Purification and sequencing of multiple forms of Brassica napus seed napin small
A;Reference number: S70336; MUID:96283790; PMID:8679670

A;Accession: S70338

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <NEU>

Query Match 41.4%; Score 24; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGW 6
|||:
Db 8 GPSW 11

RESULT 22

PH1322

Ig heavy chain DJ region (clone C344-99) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PH1322

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lympho

A;Reference number: PH1302; MUID:93094761; PMID:1460419

A;Accession: PH1322

A;Molecule type: DNA

A;Residues: 1-14 <WAS>

C;Keywords: heterotetramer; immunoglobulin

Query Match 41.4%; Score 24; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
: |||:
Db 2 WGSWG 6

RESULT 23

PT0288

Ig heavy chain CRD3 region (clone 4-106) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0288

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and jo

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0288

A;Molecule type: DNA

A;Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 39.7%; Score 23; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6
| |||:
Db 5 YSSGW 9

RESULT 24

S65388

cytochrome-c oxidase (BC 1.9.3.1) chain VII c, hepatic - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

A;Accession: S65388; S65389

R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65388
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SCH>
A;Accession: S65389
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SC2>
C;Superfamily: cytochrome-c oxidase chain VIIC
C;Keywords: oxidoreductase

Query Match 39.7%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 HY--GPG 5
|||
2 HYEGPG 8
|||

Db

RESULT 25
S77990
cytochrome-c oxidase (EC 1.9.3.1) chain VIIC - bigeye tuna (fragment)
C;Species: Thunnus obesus (bigeye tuna)
C;Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998
C;Accession: S77990
R;Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A;Reference number: S77990
A;Accession: S77990
A;Molecule type: protein
A;Residues: 1-10 <ARN>
A;Experimental source: heart; liver
C;Genetics:
A;Genome: nuclear
C;Function:
A;Pathway: oxidative phosphorylation; respiratory chain
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 39.7%; Score 23; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 HY--GPG 5
|||
2 HYEGPG 8
|||

Db

RESULT 26
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0289
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0289
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 39.7%; Score 23; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WVSM 9
|:|

Db 4 WISM 7

RESULT 27
S05002
corazonin - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Apr-1998
C;Accession: S05002
R;Veenstra, J.A.
FEBS Lett. 250, 231-234, 1989
A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american
A;Reference number: S05002; MUID:89325572; PMID:2753132
A;Accession: S05002
A;Molecule type: protein
A;Residues: 1-11 <VER>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 39.7%; Score 23; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
|:|
5 YSRGWTN 11
|:|

Db

RESULT 28
PT0302
Ig heavy chain CRD3 region (clone 5-112) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0302
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0302
A;Molecule type: DNA
A;Residues: 1-11 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 39.7%; Score 23; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6
|:|
6 YSSGW 10
|:|

Db

RESULT 29
S08995
hypertrehalosemic hormone I - oriental cockroach
N;Alternate names: Pea-CAH-I
C;Species: Blatta orientalis (oriental cockroach)
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S08995
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosemic neuropeptides isolated from the corpor
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S08995
A;Molecule type: protein
A;Residues: 1-8 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 30

A43976
adipokinetic hormone I - American cockroach
N:Alternate names: Periplaneta americana CC-1
C:Species: Periplaneta americana (American cockroach)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C:Accession: A43976
R:Scarborough, R.M.; Jamieson, G.C.; Kalish, F.; Kramer, S.J.; McEnroe, G.A.; Miller, C.
Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
A:Reference number: A43923; MUID:84238179; PMID:6591205
A:Accession: A43923
A:Molecule type: protein
A:Residues: 1-8 <SCA>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 31

A44960
neuropeptide Led-CC-I - Colorado potato beetle
C:Species: Leptinotarsa decemlineata (Colorado potato beetle)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A44960
R:Gaede, G.; Kellner, R.
Peptides 10, 1287-1289, 1989
A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle and
A:Reference number: A44960; MUID:90160053; PMID:2576128
A:Accession: A44960
A:Molecule type: protein
A:Residues: 1-8 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 32

A43976
hypertrehalosemic hormone - yellow mealworm
C:Species: Tenebrio molitor (yellow mealworm)
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C:Accession: A43976
R:Gaede, G.; Rosinski, G.

Peptides 11, 455-459, 1990
A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid bee
A:Reference number: A43976; MUID:90341081; PMID:2381871
A:Accession: A43976
A:Molecule type: protein
A:Residues: 1-8 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 33

B43976
hypertrehalosemic hormone - beetle (Zophobas rugipes)
C:Species: Zophobas rugipes
C>Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 07-May-1999
C:Accession: B43976
R:Gaede, G.; Rosinski, G.
Peptides 11, 455-459, 1990
A:Title: The primary structure of the hypertrehalosemic neuropeptide from tenebrionid bee
A:Reference number: A43976; MUID:90341081; PMID:2381871
A:Accession: B43976
A:Molecule type: protein
A:Residues: 1-8 <GAE>
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 34

A05169
neuropeptide M-I - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C:Accession: A05169
R:Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L.
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A:Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mass
A:Reference number: A90118; MUID:85046530; PMID:6548628
A:Accession: A05169
A:Molecule type: protein
A:Residues: 1-8 <WIT>
C:Keywords: neuropeptide

Query Match 37.9%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6
:: ||
Db 3 NFSPNW 8

RESULT 35

S53789

```

neuropeptide Pec-HrTH - Platyleura capensis
C;Species: Platyleura capensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C;Accession: S53789
R;Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehalose
A;Reference number: S53789; PMID:95225985; PMID:7710694
A;Accession: S53789
A;Molecule type: protein
A;Residues: 1-10 <GAE>
C;Keywords: blocked amino end; blocked carboxyl end

Query Match 37.9%; Score 22; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 7.2e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPWG 6
  : : | |
Db 3 NFSPSW 8

RESULT 36
A60409
bombesin-like peptide L - frog (Pseudophryne guentheri)
C;Species: Pseudophryne guentheri
C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C;Accession: A60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australia
A;Reference number: A60409; PMID:90287814; PMID:2356157
A;Accession: A60409
A;Molecule type: protein
A;Residues: 1-13 <SIN>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.9%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GPQW 6
  : : | |
Db 4 GPQW 7

RESULT 37
Ig kappa chain J segment (J-kappa-3) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S23640
R;Huber, C.; Klobeck, H.G.; Zachau, H.G.
Eur. J. Immunol. 22, 1561-1565, 1992
A;Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)
A;Reference number: S23637; PMID:92289816; PMID:1601042
A;Accession: S23640
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-13 <HUB>
A;Cross-references: EMBL:X63370
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
C;Keywords: heterotetramer; immunoglobulin

Query Match 37.9%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGPQ 5
  : : | |

```

Db 3 FGPG 6

RESULT 38

RHLMGS

```

gonadoliberin - sea lamprey
N;Alternate names: gonadotropin releasing hormone (GnRH)
C;Species: Petromyzon marinus (sea lamprey)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 18-Mar-1997
C;Accession: A01412
R;Sherwood, N.M.; Sower, S.A.; Marshak, D.R.; Fraser, B.A.; Brownstein, M.J.
J. Biol. Chem. 261, 4812-4819, 1986
A;Title: Primary structure of gonadotropin-releasing hormone from lamprey brain.
A;Reference number: A01412; PMID:86168192; PMID:3514603
A;Accession: A01412
A;Molecule type: protein
A;Residues: 1-10 <SHE>
A;Comment: This hormone was isolated from the brain.
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Gly) #status experimental

```

```

Query Match 36.2%; Score 21; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy 1 HYGPWG 6

: : | |

Db 2 HYSLEW 7

RESULT 39

S68649

spermadhesin AQN-3 - pig (fragments)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999

C;Accession: S68649

R;Calvete, J.J.; Dostalova, Z.; Sanz, L.; Adermann, K.; Thole, H.H.; Toepfer-Petersen, E.

FEBS Lett. 379, 207-211, 1996

A;Title: Mapping the heparin-binding domain of boar spermadhesins.

A;Reference number: S68648; PMID:96184566; PMID:8603690

A;Accession: S68649

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6;7-11 <CAL>

```

Query Match 36.2%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 5 GWV 7

: : | |

Db 5 GWV 7

RESULT 40

PT0209

T-cell receptor alpha chain V-J region (4-1-L.6) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0209

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A;Reference number: PT0209; PMID:91217621; PMID:1902501

A;Accession: PT0209

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

```

Query Match 36.2%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

```

Qy 2 YGPQ 5

: : | |

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYG 3

Db 6 HYG 8

RESULT 41

PT0274

Ig heavy chain CRD3 region (clone 3-109B) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0274

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0274

A:Molecule type: DNA

A:Residues: 1-12 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 36.2%; Score 21; DB 2; Length 12;

Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 YGPGWVS 8

Db 3 YSSSWTS 9

RESULT 42

S03530

Ig heavy chain J region (JH-4) - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000

C:Accession: S03530

R:Schwager, J.; Grossberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus

A:Reference number: S01158; MUID:89052653; PMID:2903824

A:Accession: S03530

A:Molecule type: DNA

A:Residues: 1-14 <SCH>

A:Cross-references: EMBL:X14918; NID:g64805; PIDN:CAA33043.1; PID:gl334657

Query Match

Best Local Similarity 36.2%; Score 21; DB 2; Length 14;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HVGPG 5

Db 3 HWGQG 7

RESULT 43

A28004

adipokinetic hormone G - two-spotted cricket

N:Alternate names: AKH-G

C:Species: Gryllus bimaculatus (two-spotted cricket)

C>Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997

C:Accession: A28004

R:Gaede, G.; Rinehart, K.L.

Biochem. Biophys. Res. Commun. 149, 908-914, 1987

A:Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide

A:Reference number: A28004; MUID:88106553; PMID:3426616

A:Accession: A28004

A:Molecule type: protein

A:Residues: 1-8 <GAE>

A>Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 34.5%; Score 20; DB 2; Length 8;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6

Db 3 NFSTGW 8

RESULT 44

S10596

adipokinetic hormone - pond skimmer

C:Species: Libellula auripennis

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 14-Nov-1997

C:Accession: S10596

R:Gaede, G.

Biol. Chem. Hoppe-Seyler 371, 475-483, 1990

A:Title: The putative ancestral peptide of the adipokinetic/red-pigment-concentrating hor

A:Reference number: S10596; MUID:90359055; PMID:2390213

A:Accession: S10596

A:Molecule type: protein

A:Residues: 1-8 <BIO>

C:Comment: This peptide has both adipokinetic and hypertrehalosemic activities.

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 34.5%; Score 20; DB 2; Length 8;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGW 6

Db 3 NFTPSW 8

RESULT 45

S11545

adipokinetic hormone - nestling-sucking blowfly

C:Species: Protophormia terraenovae (nestling-sucking blowfly)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 31-Oct-1997

C:Accession: S11545

R:Gaede, G.; Wilps, H.; Kellner, R.

Biochem. J. 269, 309-313, 1990

A:Title: Isolation and structure of a novel charged member of the red-pigment-concentrat

A:Reference number: S11545; MUID:90351345; PMID:2386478

A:Accession: S11545

A:Molecule type: protein

A:Residues: 1-8 <GAE>

C:Superfamily: adipokinetic hormone

C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match

Best Local Similarity 40.0%; Score 20; DB 2; Length 8;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGW 6

Db 4 RSPDW 8

Search completed: August 30, 2004, 10:58:52

Job time : 3.70608 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0068 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	14	15	US-10-394-980-52
2	31	53.4	8	10	US-09-849-092-2
3	31	53.4	11	11	US-09-791-551-99
4	30	51.7	8	10	US-09-880-748-2870
5	30	51.7	8	12	US-10-293-418-2870
6	28	48.3	8	15	US-10-186-229-90
7	28	48.3	10	14	US-10-072-419-2
8	28	48.3	11	12	US-10-417-895A-53
9	28	48.3	13	16	US-10-468-370-599
10	27.5	47.4	13	16	US-10-381-112-51
11	27.5	47.4	13	16	US-10-381-112-91
12	27.5	47.4	14	16	US-10-381-112-31
13	27.5	47.4	14	16	US-10-381-112-50
14	27.5	47.4	14	16	US-10-381-112-62
15	27	46.6	10	14	US-10-190-082-450

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16 27 46.6 11 9 US-09-861-597-12 Sequence 12, Appl
17 27 46.6 12 14 US-10-286-457-411 Sequence 411, Appl
18 26.5 45.7 8 10 US-09-863-600E-28 Sequence 28, Appl
19 26.5 45.7 11 10 US-09-863-600E-17 Sequence 17, Appl
20 26.5 45.7 11 12 US-10-609-217-429 Sequence 429, Appl
21 26.5 45.7 11 12 US-10-609-217-429 Sequence 429, Appl
22 26.5 45.7 11 12 US-10-632-388-429 Sequence 1040, Ap
23 26.5 45.7 11 12 US-10-632-388-429 Sequence 429, Appl
24 26.5 45.7 11 12 US-10-632-388-1040 Sequence 1040, Ap
25 26.5 45.7 11 12 US-10-651-723-429 Sequence 429, Appl
26 26.5 45.7 11 12 US-10-651-723-1040 Sequence 1040, Ap
27 26.5 45.7 11 12 US-10-645-761-429 Sequence 429, Appl
28 26.5 45.7 11 12 US-10-645-761-1040 Sequence 1040, Ap
29 26.5 45.7 11 16 US-10-666-696-429 Sequence 429, Appl
30 26.5 45.7 11 16 US-10-666-696-1040 Sequence 1040, Ap
31 26.5 45.7 11 16 US-10-653-048-429 Sequence 429, Appl
32 26.5 45.7 12 10 US-09-863-600E-18 Sequence 1040, Ap
33 26.5 45.7 12 10 US-09-863-600E-25 Sequence 18, Appl
34 26.5 45.7 12 12 US-10-609-217-1041 Sequence 25, Appl
35 26.5 45.7 12 12 US-10-632-388-1041 Sequence 1041, Ap
36 26.5 45.7 12 12 US-10-651-723-1041 Sequence 1041, Ap
37 26.5 45.7 12 14 US-10-271-343-14 Sequence 1041, Ap
38 26.5 45.7 12 16 US-10-666-696-1041 Sequence 14, Appl
39 26.5 45.7 12 16 US-10-653-048-1041 Sequence 1041, Ap
40 26.5 45.7 13 10 US-09-863-600E-16 Sequence 1041, Ap
41 26.5 45.7 13 12 US-10-609-217-428 Sequence 428, Appl
42 26.5 45.7 13 12 US-10-609-217-1039 Sequence 1039, Ap
43 26.5 45.7 13 12 US-10-632-388-428 Sequence 428, Appl
44 26.5 45.7 13 12 US-10-632-388-1039 Sequence 1039, Ap
45 26.5 45.7 13 12 US-10-632-388-1039 Sequence 1039, Ap
```

ALIGNMENTS

```
RESULT 1
US-10-394-980-52
; Sequence 52, Application US/10394980
; Publication No. US20040005633A1
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: part of CYPB_HUMAN (peptidyl-prolyl cis-trans isomerase B)
US-10-394-980-52
```

```
Query Match 100.0%; Score 58; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HYGPGWVSM 9
Db 1 HYGPGWVSM 9
```

RESULT 2
US-09-849-092-2
; Sequence 2, Application US/09849092
; Publication No. US20030032169A1
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
; TITLE OF INVENTION: CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
; TITLE OF INVENTION: RETINOL BINDING PROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,092
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/729,594
; FILING DATE:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/375,962
; FILING DATE: 20-January-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,418
; FILING DATE: 10-June-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20030032169A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5372.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-849-092-2
Query Match 53.4%; Score 31; DB 10; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 YPGW 6
DB 1 YSPGW 5
RESULT 3
US-09-791-551-99
; Sequence 99, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390

; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 99
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-99
Query Match 53.4%; Score 31; DB 11; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 HYGPGW 6
DB 2 HYGSSW 7
RESULT 4
US-09-880-748-2870
; Sequence 2870, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2870
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2870
Query Match 51.7%; Score 30; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GPGW 6
DB 2 GPGW 5
RESULT 5
US-10-293-418-2870
; Sequence 2870, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15

Query Match 51.7%; Score 30; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GPGW 6
DB 2 GPGW 5
RESULT 6
US-10-186-229-90
; Sequence 90, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2870

Query Match 51.7%; Score 30; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GPGW 6
DB 2 GPGW 5

RESULT 6
US-10-186-229-90
; Sequence 90, Application US/10186229
; Publication No. US20040001827A1
; GENERAL INFORMATION:
; APPLICANT: Dennis, Mark S.
; TITLE OF INVENTION: SERUM ALBUMIN BINDING PEPTIDES FOR TUMOR TARGETING
; CURRENT APPLICATION NUMBER: US/10/186,229
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides
US-10-186-229-90

Query Match 48.3%; Score 28; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PGWV 7
DB 4 PGWV 7

RESULT 7
US-10-072-419-2
; Sequence 2, Application US/10072419
; Publication No. US2003016217A1
; GENERAL INFORMATION:
; APPLICANT: Schacter, Bernice
; APPLICANT: Schacter, Lee
; TITLE OF INVENTION: Compositions and Methods for Promoting Lipid Mobilization in Human
; FILE REFERENCE: 10739-1
; CURRENT APPLICATION NUMBER: US/10/072,419
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Gromphadorhina portentosa
US-10-072-419-2

Query Match 48.3%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYGPWG 6
DB 3 NFSPGW 8

RESULT 8
US-10-417-895A-53
; Sequence 53, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-53

Query Match 48.3%; Score 28; DB 12; Length 11;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HYGPWVS 8
DB 2 YYGSSWYS 9

RESULT 9
US-10-468-370-539
; Sequence 599, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 599

```
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-599
```

```
Query Match      48.3%; Score 28; DB 16; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 GPGWV 7
        |||||
Db       8 GPNWV 12
```

```
RESULT 10
US-10-381-112-51
; Sequence 51, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 51
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 13
; OTHER INFORMATION: C-terminal amidation
US-10-381-112-51
```

```
Query Match      47.4%; Score 27.5; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      3 GP-GWVSM 9
        |||||
Db       6 GPWGWVCM 13
```

```
RESULT 11
US-10-381-112-91
; Sequence 91, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
```

```
; SEQ ID NO 91
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IGE receptor binding peptide described in Example 6
US-10-381-112-91
```

```
Query Match      47.4%; Score 27.5; DB 16; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      3 GP-GWVSM 9
        |||||
Db       6 GPWGWVCM 13
```

```
RESULT 12
US-10-381-112-31
; Sequence 31, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 31
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: clone g3c.21 shown in Table 4
US-10-381-112-31
```

```
Query Match      47.4%; Score 27.5; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
QY      3 GP-GWVSM 9
        |||||
Db       4 GPWGWVCM 11
```

```
RESULT 13
US-10-381-112-50
; Sequence 50, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasnik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 50
; LENGTH: 14
; TYPE: PRT
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ige receptor binding peptide of Table 5. IgE068
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 14
; OTHER INFORMATION: C-terminal amidation
US-10-381-112-50

Query Match 47.4%; Score 27.5; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 GP-GWVSM 9
Db 7 GPWGVCVM 14

RESULT 14
US-10-381-112-82
; Sequence 82, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovasinik, Melissa A.
; TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595
; SEQ ID NO 82
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ige receptor binding peptide of Table 5. IgE107
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: N-terminal acetylation
US-10-381-112-82

Query Match 47.4%; Score 27.5; DB 16; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 3 GP-GWVSM 9
Db 7 GPWGVCVM 14

RESULT 15
US-10-190-082-450
; Sequence 450, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHASE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 450

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-450

Query Match 46.6%; Score 27; DB 14; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PGWVSM 9
Db 3 PGWWSL 8

RESULT 16
US-09-861-597-12
; Sequence 12, Application US/09861597
; Patent No. US20020064539A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPPE, Michel
; APPLICANT: GARSON, Jean-Claude
; APPLICANT: ARRAUDEAU, Jean-Pierre
; TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
; TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
; TITLE OF INVENTION: ANALOG
; FILE REFERENCE: 6388-0365-0
; CURRENT APPLICATION NUMBER: US/09/861,597
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/247,806
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: FR 98/01614
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa corresponds to the amino acid sequence GPS or
; OTHER INFORMATION: GPG
; OTHER INFORMATION: Description of Artificial Sequence:protein
US-09-861-597-12

Query Match 46.6%; Score 27; DB 9; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YPGGWVS 8
Db 4 YGPGQXS 10

RESULT 17
US-10-286-457-411
; Sequence 411, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 411
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
;
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-411

Query Match      46.6%; Score 27; DB 14; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 HYGPGWVS 8
   |  |  |  |
Db 3 HQASGWTS 10

RESULT 18
US-09-863-600E-28
; Sequence 17, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael, Carlos
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-28

Query Match      45.7%; Score 26.5; DB 10; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
   |  |  |  |
Db 1 HFGELTW 8

RESULT 19
US-09-863-600E-17
; Sequence 17, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-17

Query Match      45.7%; Score 26.5; DB 10; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
   |  |  |  |
Db 3 HFGELTW 10

RESULT 20
US-10-609-217-429
; Sequence 429, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-429

Query Match      45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
   |  |  |  |
Db 3 HFGELTW 10

RESULT 21
US-10-609-217-1040
; Sequence 1040, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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;
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-17

Query Match      45.7%; Score 26.5; DB 10; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
   |  |  |  |
Db 3 HFGELTW 10

RESULT 20
US-10-609-217-429
; Sequence 429, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-429

Query Match      45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPGWV 7
   |  |  |  |
Db 3 HFGELTW 10

RESULT 21
US-10-609-217-1040
; Sequence 1040, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
Db 3 HFGPLTW 10

RESULT 22

US-10-632-388-429
; Sequence 429, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
Db 3 HFGPLTW 10

RESULT 23

US-10-632-388-1040
; Sequence 1040, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE

US-10-632-388-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
Db 3 HFGPLTW 10

RESULT 24

US-10-651-723-429
; Sequence 429, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
Db 3 HFGPLTW 10

RESULT 25

US-10-651-723-1040
; Sequence 1040, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 26
US-10-645-761-429
; Sequence 429, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-645-761-429

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 27
US-10-645-761-1040
; Sequence 1040, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-645-761-1040

Query Match 45.7%; Score 26.5; DB 12; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 28
US-10-666-696-429
; Sequence 429, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-666-696-429

Query Match 45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 29
US-10-666-696-1040
; Sequence 1040, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT


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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO MIMETIC PEPTIDE
US-10-666-696-1040

Query Match      45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 30
US-10-653-048-429
; Sequence 429, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-429

Query Match      45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 31
US-10-653-048-1040
; Sequence 1040, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-1040

Query Match      45.7%; Score 26.5; DB 16; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 32
US-09-863-600E-18
; Sequence 18, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-18

Query Match      45.7%; Score 26.5; DB 10; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 33
US-09-863-600E-25
; Sequence 25, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-25

Query Match          45.7%; Score 26.5; DB 10; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 HYGP-GWV 7
      |:|:|:|
Db      4 HFGPLTWV 11

RESULT 34
US-10-609-217-1041
; Sequence 1041, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-1041

Query Match          45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 HYGP-GWV 7
      |:|:|:|
Db      3 HFGPLTWV 10

RESULT 35
US-10-632-388-1041
; Sequence 1041, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-1041

Query Match          45.7%; Score 26.5; DB 10; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 HYGP-GWV 7
      |:|:|:|
Db      4 HFGPLTWV 11

RESULT 36
US-10-651-723-1041
; Sequence 1041, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-1041

Query Match          45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 HYGP-GWV 7
      |:|:|:|
Db      3 HFGPLTWV 10

RESULT 37
US-10-645-761-1041
; Sequence 1041, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-645-761-1041
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Query Match 45.7%; Score 26.5; DB 12; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 38
US-10-271-343-14
; Sequence 14, Application US/10271343
; Publication No. US20030166003A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas J.
; APPLICANT: Stavovskanik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; FILE OF INVENTION: ON PHAGE
; FILE REFERENCE: 11669.116US11
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
US-10-271-343-14

Query Match 45.7%; Score 26.5; DB 14; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 39
US-10-666-696-1041
; Sequence 1041, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide

; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-666-696-1041

Query Match 45.7%; Score 26.5; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 40
US-10-653-048-1041
; Sequence 1041, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-1041

Query Match 45.7%; Score 26.5; DB 16; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 HYGP-GWV 7
Db 3 HFGPLTWV 10

RESULT 41
US-09-863-600E-16
; Sequence 16, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide

US-09-863-600E-16

Query Match 45.7%; Score 26.5; DB 10; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 42

US-10-609-217-428
; Sequence 428, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 428
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-428

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 43

US-10-609-217-1039
; Sequence 1039, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1039
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-609-217-1039

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 44

US-10-632-388-428
; Sequence 428, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 428
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-428

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGp-GWV 7
|:|:|
Db 4 HFGPLTWV 11

RESULT 45

US-10-632-388-1039
; Sequence 1039, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1039
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-632-388-1039

Query Match 45.7%; Score 26.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYG-GRV 7
|:| |
Db 4 HFGPLTW 11

Search completed: August 30, 2004, 11:05:00
Job time : 12.0068 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

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Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
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Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	58.6	14	5	PCT-US93-06751-120
2	32	55.2	8	1	US-08-271-830-56
3	31	53.4	8	1	US-08-375-962B-2
4	31	53.4	8	2	US-08-562-114B-2
5	31	53.4	8	3	US-08-729-594A-2
6	31	53.4	8	4	US-08-937-993-2
7	30	51.7	13	5	PCT-US93-06751-66
8	30	51.7	14	5	PCT-US93-06751-93
9	29	50.0	11	6	5164481-10
10	29	50.0	14	5	PCT-US93-06751-65
11	28	48.3	10	1	US-08-353-400-26
12	28	48.3	10	2	US-08-747-137-122
13	28	48.3	11	2	US-08-598-873-68
14	28	48.3	11	3	US-08-605-430-68
15	28	48.3	12	2	US-08-406-330-33
16	28	48.3	12	2	US-08-556-597-33
17	28	48.3	14	5	PCT-US93-06751-67
18	28	48.3	14	5	PCT-US93-06751-103
19	27	46.6	11	2	US-08-665-202-97
20	27	46.6	11	2	US-08-665-202-105
21	27	46.6	11	3	US-09-247-806-12
22	27	46.6	11	4	US-09-315-574-97
23	27	46.6	11	4	US-09-315-574-105
24	27	46.6	13	5	PCT-US93-06751-102
25	27	46.6	14	5	PCT-US93-06751-63
26	26.5	45.7	8	1	US-08-484-635-201
27	26.5	45.7	8	2	US-08-484-631-201

28 26.5 45.7 8 2 US-08-827-570-201
29 26.5 45.7 11 1 US-08-484-135-17
30 26.5 45.7 11 1 US-08-484-635-17
31 26.5 45.7 11 2 US-08-484-631-17
32 26.5 45.7 11 2 US-08-827-570-17
33 26.5 45.7 11 3 US-08-905-310-11
34 26.5 45.7 11 4 US-09-428-082B-429
35 26.5 45.7 11 4 US-09-428-082B-1040
36 26.5 45.7 12 1 US-08-484-135-18
37 26.5 45.7 12 1 US-08-484-635-200
38 26.5 45.7 12 1 US-08-484-635-246
39 26.5 45.7 12 2 US-08-484-631-200
40 26.5 45.7 12 2 US-08-827-570-200
41 26.5 45.7 12 2 US-08-827-570-246
42 26.5 45.7 12 3 US-08-786-690-3
43 26.5 45.7 12 4 US-09-428-082B-1041
44 26.5 45.7 13 1 US-08-484-135-16
45 26.5 45.7 13 1 US-08-484-135-16

ALIGNMENTS

RESULT 1
PCT-US93-06751-120
; Sequence 120, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
; TITLE OF INVENTION: Immunological Conjugates of OMPC and
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06751
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Beta
PCT-US93-06751-120

Query Match 58.6%; Score 34; DB 5; Length 14;
Best Local Similarity 100.0%; Pred.No. 23;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYPGW 5
|||||

Db

7 HYPGP 11

RESULT 2

US-08-271-830-56
; Sequence 56, Application US/08271830
; Patent No. 5510332
; GENERAL INFORMATION:
; APPLICANT: Kogan, Timothy P.
; APPLICANT: Ren, Kaijun
; APPLICANT: Vanderslice, Peter
; APPLICANT: Beck, Pamela J.
; TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
; TITLE OF INVENTION: INTEGRIN 'A 1 TO VCAM OR FIBRONECTIN AND
; TITLE OF INVENTION: LINEAR PEPTIDES THEREFOR
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 5510332th Statson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271.830
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5510332thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 8
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "Xaa=Pro-NH2."

US-08-271-830-56

Query Match

Best Local Similarity 55.2%; Score 32; DB 1; Length 8;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy

3 GPGWVSM 9

Db

1 GPGWLDV 7

RESULT 3

US-08-375-962B-2
; Sequence 2, Application US/08375962B
; Patent No. 5731195
; GENERAL INFORMATION:
; APPLICANT: SIMON, ANDRAS; HELLMAN, ULF; WERNSTEDT,
; APPLICANT: CRISTER, ERIKSSON, ULF.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecule
; TITLE OF INVENTION: Which Codes for A 32 kDa Protein Having 11-CIS Retinol
; TITLE OF INVENTION: Dehydrogenase Activity, and Which Associates With P63,
; TITLE OF INVENTION: A Portion of a Retinol Binding Protein Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/258,418
FILING DATE: 6-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-375-962B-2

Query Match

Best Local Similarity 53.4%; Score 31; DB 1; Length 8;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

2 YPGW 6

Db

1 YPGW 5

RESULT 4

US-08-562-114B-2
; Sequence 2, Application US/08562114B
; Patent No. 5972646
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON ET AL.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A
; TITLE OF INVENTION: 32 KDA PROTEIN HAVING 11-CIS RETINOL HYDROGENASE
; TITLE OF INVENTION: ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
; TITLE OF INVENTION: PORTION OF A RETINOL BINDING PROTEIN RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/562,114B
FILING DATE: 22-No. 5972646ember-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet

REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5372.2 CIP
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-562-114B-2

Query Match 53.4%; Score 31; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSPGW 6
DB 1 YSPGW 5

RESULT 5

US-08-729-594A-2
Sequence 2, Application US/08729594A
Patent No. 6280997
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE WHICH
CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASE
ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
RETINOL BINDING PROTEIN RECEPTOR
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pelfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,594A
FILING DATE: 11-October-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6280997ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No 6280997man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5372.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-729-594A-2

Query Match 53.4%; Score 31; DB 3; Length 8;

Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSPGW 6
DB 1 YSPGW 5

RESULT 6

US-08-937-993-2
Sequence 2, Application US/08937993
Patent No. 6399344
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf; Simon, Andras; Romert, Anna
TITLE OF INVENTION: ISOLATED PROTEINS HAVING CIS-R
DEHYDROGENASE ACTIVITY
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,993
FILING DATE: September 26, 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/729,594
FILING DATE: 11-October-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/562,114
FILING DATE: 22-No. 6399344ember-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/375,962
FILING DATE: 20-January-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6399344man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-937-993-2

Query Match 53.4%; Score 31; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSPGW 6
DB 1 YSPGW 5

RESULT 7

PCT-US93-06751-66
Sequence 66, Application PC/TUS9306751
GENERAL INFORMATION:
APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold

;; TITLE OF INVENTION: Immunological Conjugates of OMPC and
;; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
;; NUMBER OF SEQUENCES: 146
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Merck & Co., Inc.
;; STREET: P.O. Box 2000
;; CITY: Rahway
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07065
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/06751
;; FILING DATE: 19930719
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meredith, Roy D.
;; REGISTRATION NUMBER: 30,777
;; REFERENCE/DOCKET NUMBER: 18614
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (908) 594-4678
;; TELEFAX: (908) 594-4720
;; TELEX: 138825
;; INFORMATION FOR SEQ ID NO: 66:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-66

Query Match 51.7%; Score 30; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 92;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPG 5
|:|:|
Db 4 HFGPG 8

RESULT 8
PCT-US93-06751-93
;; Sequence 93, Application PC/TUS9306751
;; GENERAL INFORMATION:
;; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
;; TITLE OF INVENTION: Immunological Conjugates of OMPC and
;; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
;; NUMBER OF SEQUENCES: 146
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Merck & Co., Inc.
;; STREET: P.O. Box 2000
;; CITY: Rahway
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07065
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/06751
;; FILING DATE: 19930719
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:

;; NAME: Meredith, Roy D.
;; REGISTRATION NUMBER: 30,777
;; REFERENCE/DOCKET NUMBER: 18614
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (908) 594-4678
;; TELEFAX: (908) 594-4720
;; TELEX: 138825
;; INFORMATION FOR SEQ ID NO: 93:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; IMMEDIATE SOURCE: Random Epitope Library Gamma
PCT-US93-06751-93

Query Match 51.7%; Score 30; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 99;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPG 5
|:|:|
Db 4 HFGPG 8

RESULT 9
5164481-10
;; Patent No. 5164481
;; APPLICANT: LACROIX, MARTIAL; ZREIN, MAAN; DIONNE, GERVAIS
;; TITLE OF INVENTION: PEPTIDES AND ANALOGUES AND MIXTURES
;; FOR DETECTING AND ELICITING ANTIBODIES TO RUBELLA VIRUS
;; NUMBER OF SEQUENCES: 11
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/397,767
;; FILING DATE: 23-AUG-1989
;; SEQ ID NO: 10:
;; LENGTH: 11
5164481-10

Query Match 50.0%; Score 29; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YGPGWS 8
|:|:|
Db 2 HGPDMAS 8

RESULT 10
PCT-US93-06751-65
;; Sequence 65, Application PC/TUS9306751
;; GENERAL INFORMATION:
;; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold
;; TITLE OF INVENTION: Immunological Conjugates of OMPC and
;; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
;; NUMBER OF SEQUENCES: 146
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Merck & Co., Inc.
;; STREET: P.O. Box 2000
;; CITY: Rahway
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07065
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/06751

;
; FILING DATE: 19930719
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 18614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; TELEX: 138925
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-65

Query Match 50.0%; Score 29; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYPGW 5
|:|
DB 4 HWPGW 8

RESULT 11
US-08-353-400-26
; Sequence 26, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-26

Query Match 48.3%; Score 28; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYPGW 6
|:|
DB 4 HRGSW 9

RESULT 12

US-08-747-137-122
; Sequence 122, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: Yen, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-0008400S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "p-Glu"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "Thr-Amide"
US-08-747-137-122

Query Match 48.3%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYPGW 6
::|
DB 3 NFPGW 8

RESULT 13
US-08-598-873-68
; Sequence 68, Application US/08598873
; Patent No. 5928884
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.

```
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; METHODS BASED THEREON
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/598,873
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-598-873-68

Query Match 48.3%; Score 28; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 4
DB 1 HYGP 4

RESULT 14
US-08-605-430-68
; Sequence 68, Application US/08605430
; Patent No. 6242212
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo M.
; APPLICANT: Huebner, Kay
; TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
; METHODS BASED THEREON
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/605,430
; FILING DATE: 22-FEB-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
```

```
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8666-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-605-430-68

Query Match 48.3%; Score 28; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 4
DB 1 HYGP 4

RESULT 15
US-08-406-330-33
; Sequence 33, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lytle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-330-33

Query Match 48.3%; Score 28; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGWV 7
DB 3 FGPFVW 8
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; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-103

Query Match      48.3%; Score 28; DB 5; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HYGPG 5
Db      4 YGPG 8

RESULT 19
US-08-665-202-97
; Sequence 97, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 13-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-97

Query Match      46.6%; Score 27; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HYGPGW 7
Db      5 YRSGW 11

RESULT 20
US-08-665-202-97
; Sequence 97, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 13-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-97

Query Match      46.6%; Score 27; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HYGPGW 7
Db      5 YRSGW 11

RESULT 21
US-09-247-806-12
; Sequence 12, Application US/09247806
; Patent No. 6280747
; GENERAL INFORMATION:
; APPLICANT: PHILLIPPE, Michel
; APPLICANT: GARSON, Jean-Claude
; APPLICANT: ARRAUDEAU, Jean-Pierre
; TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
; TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
; TITLE OF INVENTION: ANALOG
; FILE REFERENCE: 6388-0365-0
; CURRENT APPLICATION NUMBER: US/09/247,806
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: FR 98/01614
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 14
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US-08-665-202-105
; Sequence 105, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 13-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-105

Query Match      46.6%; Score 27; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HYGPGW 7
Db      5 YRSGW 11

RESULT 21
US-09-247-806-12
; Sequence 12, Application US/09247806
; Patent No. 6280747
; GENERAL INFORMATION:
; APPLICANT: PHILLIPPE, Michel
; APPLICANT: GARSON, Jean-Claude
; APPLICANT: ARRAUDEAU, Jean-Pierre
; TITLE OF INVENTION: COSMETIC OR DERMATOLOGICAL COMPOSITION CONTACTING AT
; TITLE OF INVENTION: LEAST ONE NATURAL OR RECOMBINANT SPIDER SILK OR AN
; TITLE OF INVENTION: ANALOG
; FILE REFERENCE: 6388-0365-0
; CURRENT APPLICATION NUMBER: US/09/247,806
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: FR 98/01614
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 14
```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xaa corresponds to the amino acid sequence GPS or
; OTHER INFORMATION: GPG
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:protein
US-09-247-806-12

Query Match 46.6%; Score 27; DB 3; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YGPGWVS 8
:|:|:|:|
Db 4 YGPGQXS 10

RESULT 22
US-09-315-574-97
; Sequence 97, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; APPLICATION NUMBER: US 08/665,202
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-97

Query Match 46.6%; Score 27; DB 4; Length 11;

Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HYPGGW 7
:|:|:|:|
Db 5 YYRSGW 11

RESULT 23
US-09-315-574-105
; Sequence 105, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; APPLICATION NUMBER: US 08/665,202
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 105:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-574-105

Query Match 46.6%; Score 27; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYPGGW 7
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Db 5 YYRSGW 11

RESULT 24
PCT-US93-06751-102
; Sequence 102, Application PC/TUS9306751
; GENERAL INFORMATION:
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold

;/ TITLE OF INVENTION: Immunological Conjugates of OMPC and
;/ TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
;/ NUMBER OF SEQUENCES: 146
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Merck & Co., Inc.
;/ STREET: P.O. Box 2000
;/ CITY: Rahway
;/ STATE: NJ
;/ COUNTRY: USA
;/ ZIP: 07065
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/06751
;/ FILING DATE: 19930719
;/ CLASSIFICATION:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Meredith, Roy D.
;/ REGISTRATION NUMBER: 30,777
;/ REFERENCE/DOCKET NUMBER: 18614
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (908) 594-4678
;/ TELEFAX: (908) 594-4720
;/ TELEX: 138825
;/ INFORMATION FOR SEQ ID NO: 102:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 13 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ HYPOTHETICAL: NO
;/ ANTI-SENSE: NO
;/ IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-102

Query Match 46.6%; Score 27; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPG 5
Db 4 NYGPG 8

RESULT 25
PCT-US93-06751-63
;/ Sequence 63, Application PC/TUS9306751
;/ GENERAL INFORMATION:
;/ APPLICANT: P. Keller, A. J. Conley, A. R. Shaw, B. A. Arnold
;/ TITLE OF INVENTION: Immunological Conjugates of OMPC and
;/ TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes
;/ NUMBER OF SEQUENCES: 146
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Merck & Co., Inc.
;/ STREET: P.O. Box 2000
;/ CITY: Rahway
;/ STATE: NJ
;/ COUNTRY: USA
;/ ZIP: 07065
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/06751
;/ FILING DATE: 19930719
;/ CLASSIFICATION:
;/ ATTORNEY/AGENT INFORMATION:

;/ NAME: Meredith, Roy D.
;/ REGISTRATION NUMBER: 30,777
;/ REFERENCE/DOCKET NUMBER: 18614
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (908) 594-4678
;/ TELEFAX: (908) 594-4720
;/ TELEX: 138825
;/ INFORMATION FOR SEQ ID NO: 63:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ HYPOTHETICAL: NO
;/ ANTI-SENSE: NO
;/ IMMEDIATE SOURCE: Random Epitope Library Delta
PCT-US93-06751-63

Query Match 46.6%; Score 27; DB 5; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HYGPGWV 7
Db 4 HLGPGRV 10

RESULT 26
US-08-484-635-201
;/ Sequence 201, Application US/08484635
;/ Patent No. 5773569
;/ GENERAL INFORMATION:
;/ APPLICANT: Wrighton, Nicholas C.
;/ APPLICANT: Dower, William J.
;/ APPLICANT: Chang, Ray S.
;/ APPLICANT: Kashyap, Arun K.
;/ APPLICANT: Jolliffe, Linda K.
;/ APPLICANT: Johnson, Dana
;/ APPLICANT: Mulcahy, Linda
;/ TITLE OF INVENTION: Compounds and Peptides That Bind to the
;/ TITLE OF INVENTION: Erythropoietin Receptor
;/ NUMBER OF SEQUENCES: 259
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Townsend and Townsend and Crew
;/ STREET: One Market Plaza, Steuart Street Tower
;/ CITY: San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94105-1492
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/484,635
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/155,940
;/ FILING DATE: 19-NOV-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Garrett-Wackowski, Eugenia
;/ REGISTRATION NUMBER: 37,330
;/ REFERENCE/DOCKET NUMBER: 16528A-43-1-1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (415) 543-9600
;/ TELEFAX: (415) 543-5043
;/ INFORMATION FOR SEQ ID NO: 201:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid


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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-201

Query Match          45.7%; Score 26.5; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPG-GWV 7
Db 1 HFGPLTWV 8

RESULT 27
US-08-484-631-201
; Sequence 201, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-201

Query Match          45.7%; Score 26.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPG-GWV 7
Db 1 HFGPLTWV 8

RESULT 28
US-08-827-570-201
; Sequence 201, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-201

Query Match          45.7%; Score 26.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGPG-GWV 7
Db 1 HFGPLTWV 8

RESULT 29
US-08-484-135-17
; Sequence 17, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. DiGiglio
; STREET: 400 Garden City Plaza
```

; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A..
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-135-17

Query Match 45.7%; Score 26.5; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
|:|:|:|
Db 3 HFGELTWW 10

RESULT 30
US-08-484-635-17
; Sequence 17, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashvap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:

; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-17

Query Match 45.7%; Score 26.5; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGp-GWV 7
|:|:|:|
Db 3 HFGELTWW 10

RESULT 31
US-08-484-631-17
; Sequence 17, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashvap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-17

Query Match 45.7%; Score 26.5; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| ||
Db 3 HFGPLTWV 10

RESULT 32

US-08-827-570-17
; Sequence 17, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-17

Query Match 45.7%; Score 26.5; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| ||
Db 3 HFGPLTWV 10

RESULT 33

US-08-905-310-11

; Sequence 11, Application US/08905310
; Patent No. 6077939
; GENERAL INFORMATION:
; APPLICANT: Wei, Ziping
; APPLICANT: Menon-Rudolph, Sunitha
; APPLICANT: Ghosh-Dastidar, Pradipt
; TITLE OF INVENTION: Polypeptides Having a Single Covalently Bound
; TITLE OF INVENTION: N-Terminal Water-Soluble Polymer, and Related Methods,
; TITLE OF INVENTION: Compositions and Kits
; FILE REFERENCE: SEQUENCE LISTING ORT 843
; CURRENT APPLICATION NUMBER: US/08/905,310
; CURRENT FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide fragment
US-08-905-310-11

Query Match 45.7%; Score 26.5; DB 3; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| ||
Db 3 HFGPLTWV 10

RESULT 34

US-09-428-082B-429
; Sequence 429, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 429
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-429

Query Match 45.7%; Score 26.5; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| ||
Db 3 HFGPLTWV 10

RESULT 35

US-09-428-082B-1040
; Sequence 1040, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.

APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-1040

Query Match 45.7%; Score 26.5; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 36
US-08-484-135-18
; Sequence 18, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivvin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. Digiglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A..
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-135-18

Query Match 45.7%; Score 26.5; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| |

Db 3 HFGPLTWV 10
RESULT 37
US-08-484-635-200
; Sequence 200, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-200

Query Match 45.7%; Score 26.5; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 38
US-08-484-635-246
; Sequence 246, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana

```

; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-246

Query Match 45.7%; Score 26.5; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 4 HEGPLTWV 11

RESULT 39
US-08-484-631-200
; Sequence 200, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-246
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-200

Query Match 45.7%; Score 26.5; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYGP-GWV 7
Db 3 HEGPLTWV 10

RESULT 40
US-08-484-631-246
; Sequence 246, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-200
```

; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-246

Query Match 45.7%; Score 26.5; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:| |
Db 4 HFGPLTWV 11

RESULT 41

US-08-827-570-200
; Sequence 200, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-200

Query Match 45.7%; Score 26.5; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
Qy 1 HYGP-GWV 7
|:|:| |
Db 3 HFGPLTWV 10

RESULT 42

US-08-827-570-246
; Sequence 246, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-246

Query Match 45.7%; Score 26.5; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 HYGP-GWV 7
|:|:| |
Db 4 HFGPLTWV 11

RESULT 43

US-08-786-690-3
; Sequence 3, Application US/087866690
; Patent No. 6221608

GENERAL INFORMATION:
APPLICANT: Middleton, Steven
APPLICANT: Johnson, Dana
APPLICANT: McMahon, Frank
APPLICANT: Mulcahy, Linda
APPLICANT: Jolliffe, Linda
TITLE OF INVENTION: METHOD FOR PURIFICATION AND USE OF
ERYTHROPOIETIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,690
FILING DATE: 08 August 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-821
TELEPHONE: 732-524-2806
TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
US-08-786-690-3

Query Match 45.7%; Score 26.5; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYG-P-GWV 7
Db 3 HFGPLTWV 10

RESULT 44
US-09-428-082B-1041
Sequence 1041, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-PA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1041
LENGTH: 12
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-09-428-082B-1041

Query Match 45.7%; Score 26.5; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYG-P-GWV 7
Db 3 HFGPLTWV 10

RESULT 45

US-08-484-135-16
Sequence 16, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. DiGiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-16

Query Match 45.7%; Score 26.5; DB 1; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 HYG-P-GWV 7
Db 4 HFGPLTWV 11

Search completed: August 30, 2004, 10:57:18
Job time : 4.55743 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4088 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-8
Perfect score: 58
Sequence: 1 HYGPGWVSM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 29Jan04: *
1: genesep1980s: *
2: genesep1990s: *
3: genesep2000s: *
4: genesep2001s: *
5: genesep2002s: *
6: genesep2003as: *
7: genesep2003bs: *
8: genesep2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	58	100.0	9	3 AAY69928	Human cyp
2	58	100.0	14	6 ABP74769	Proteome
3	49	84.5	10	3 AAY69947	Human cyp
4	49	84.5	10	6 ABR84352	Human cyp
5	45	77.6	11	3 AAY69925	Human cyp
6	34	58.6	14	2 AAR47787	HIV epit
7	32	55.2	8	2 AAR95759	Alpha-4Be
8	31	53.4	8	2 AAR88101	Bovine p3
9	31	53.4	8	2 AAM18339	Bovine p3
10	31	53.4	8	2 AAY01990	Tryptic p
11	30	51.7	8	5 ABP46859	Human Bly
12	30	51.7	9	1 AAR95363	Variable
13	30	51.7	9	2 AAR31288	HIV princ
14	30	51.7	9	2 AAR30043	HIV princ
15	30	51.7	9	2 AAR26724	HIV-FND-p
16	30	51.7	11	5 AAU98826	Adenoviru
17	30	51.7	12	5 AAU83484	PPV Vluu
18	30	51.7	13	2 AAR47733	HIV epit
19	30	51.7	14	2 AAR47760	HIV epit
20	29	50.0	10	7 ADD94624	Human SIM
21	29	50.0	14	2 AAR47732	HIV epit
22	29	50.0	14	4 AAM98717	Human pep
23	28	48.3	8	4 ABB45010	Human alb
24	28	48.3	10	2 AAR76078	Phage dis
25	28	48.3	10	2 AAY31073	Non-cross

26	28	48.3	10	7 ADC07128	Giant Mad
27	28	48.3	12	2 AAW32655	Human pla
28	28	48.3	12	2 AAW71785	Mimotope
29	28	48.3	13	5 AAE27766	Human bet
30	28	48.3	14	2 AAR47734	HIV epit
31	28	48.3	14	2 AAR47770	HIV epit
32	28	48.3	14	3 AAY57711	Rat clust
33	27.5	47.4	13	5 ABG66144	IGE Recps
34	27.5	47.4	13	5 ABG66104	IGE Recps
35	27.5	47.4	14	5 ABG66135	IGE Recps
36	27.5	47.4	14	5 ABG66084	IGE Recps
37	27.5	47.4	14	5 ABG66103	IGE Recps
38	27	46.6	8	6 AAE34589	Phage pep
39	27	46.6	9	4 AAB70713	Human TAA
40	27	46.6	10	2 AAR31271	HIV princ
41	27	46.6	10	2 AAR31308	Cyclic HI
42	27	46.6	10	2 AAR26707	HIV-PND-P
43	27	46.6	11	2 AAW08545	C6 human
44	27	46.6	11	2 AAW08535	C6 human
45	27	46.6	12	7 ADC44682	Endotheli

ALIGNMENTS

RESULT 1
AAY69928
ID AAY69928 standard; peptide; 9 AA.
XX
AC AAY69928;
XX
DT 11-APR-2000 (first entry)
XX
DE Human cyclophilin B peptide fragment #8.
XX
KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
OS Homo sapiens.
XX
PN WO9967288-A1.
XX
PD 29-DEC-1999.
XX
PF 24-JUN-1999; 99WO-JP003360.
XX
PR 25-JUN-1998; 98JP-00178449.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
PI Itoh K, Gomi S;
DR WPI; 2000-116932/10.
XX
PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
PS Claim 4; Page 51; 64pp; Japanese.
XX
CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 58; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPGWVSM 9
|||||

Db 1 HYGPGWVSM 9
1 HYGPGWVSM 9

RESULT 2
ABP74769
ID ABP74769 standard; peptide; 14 AA.
AC ABP74769;
XX
DT 03-FEB-2003 (first entry)
XX
DE Proteome analysis related peptide #54.
XX
DE Proteome analysis; isolation; determination; diagnostic assay; detection;
KW protein marker; identification; metastatic; invasive cancer;
KW differential expression; signalling pathway; chromatography.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200277016-A2.
XX
XX
XX 03-OCT-2002.
XX
XX 22-MAR-2002; 2002WO-EP003368.
XX
XX 22-MAR-2001; 2001US-0278171P.
XX 12-SEP-2001; 2001US-0318749P.
XX 20-SEP-2001; 2001US-0323999P.
XX
XX (VLAAs-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
XX Vandekerckhove J, Gevaert K;
XX
XX WPI; 2003-067379/06.
XX
XX
XX Method for isolation of peptides from complex mixture of peptides
PT involves specific chemical and/or enzymatic alteration of at least one
PT type of peptide.
XX
XX Example 20; Page 141; 193pp; English.
XX
XX The present invention describes a method (M1) for the isolation of a
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
CC separating the protein peptide mixture into fractions of peptides via
CC chromatography; (b) chemically, or enzymatically, or chemically and
CC enzymatically, altering at least one amino acid of at least one of the
CC peptides in each fraction, thereby generating a subset of altered
CC peptides; and (c) isolating the altered (flagged) peptides out of each
CC fraction via chromatography, where the chromatography of steps (a) and
CC (c) is performed with the same type of chromatography. M1 can be used for
CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in
CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular
CC changes in cells with physiological changes such as metabolic shift, in
CC the identification of biomarkers in cancers and in the identification of
CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
CC invention
XX
XX Sequence 14 AA;
XX
XX Query Match 100.0%; Score 58; DB 6; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.0059;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPGWVSM 9
1 HYGPGWVSM 9

Db 1 HYGPGWVSM 9
1 HYGPGWVSM 9

RESULT 3
AAY69947
ID AAY69947 standard; peptide; 10 AA.
XX
XX AAY69947;
AC
XX
DT 11-APR-2000 (first entry)
XX
XX Human cyclophilin B peptide fragment #27.
XX
XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.
XX
XX Homo sapiens.
OS
OS WO9967288-A1.
XX
XX 29-DEC-1999.
PD
XX 24-JUN-1999; 99WO-JP003360.
PF
XX 25-JUN-1998; 98JP-00178449.
PR
XX (SUMU) SUMITOMO PHARM CO LTD.
XX (ITOH/) ITOH K.
XX
XX Itoh K, Gomi S;
PI
XX WPI; 2000-116932/10.
DR
XX
XX Tumour antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
PT
XX Claim 4; Page 56; 64pp; Japanese.
PS
XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours
XX
XX Sequence 10 AA;
XX
XX Query Match 84.5%; Score 49; DB 3; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYGPGWV 7
1 HYGPGWV 10

Db 1 HYGPGWV 7
1 HYGPGWV 10

RESULT 4
ABR84352
ID ABR84352 standard; peptide; 10 AA.
XX
XX ABR84352;
AC
XX
DT 06-NOV-2003 (first entry)
XX
XX Human CypB HLA-A2 epitope, SEQ ID NO:3.
DE
XX Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
KW human; human leukocyte antigen; HLA-A2 epitope.
XX
XX Homo sapiens.
OS
XX

PN	JP200235286-A.
XX	
XX	18-DEC-2002.
XX	
PF	18-SEP-2001; 2001JP-00283413.
XX	
PR	13-NOV-2000; 2000JP-00345094.
XX	
PA	(ITOX/) ITO Y.
XX	
DR	WPI; 2003-508315/48.

A detection method of antigen specific T-cells, comprises the use of
 plural antigenic peptides, useful in semi-quantitative determination of
 cancer specific T-cell frequencies and for monitoring cellular immunity.
 Example 7; Page 8; 18pp; Japanese.

The invention relates to a method for the detection of antigen specific T-cells in a blood sample involving the use of a plurality of antigenic peptides. The method comprises sampling of peripheral blood monocytes; stimulation of the collected peripheral blood monocytes with antigens without direct use of antigen presenting cells; and detection of T-cells specific to the antigen in the stimulated monocytes. The method is particularly used for the detection of cancer as it can be used in semi-quantitative determination of cancer specific T-cells. It can also be used for cancer vaccine therapy for patients with cervical or prostate cancer. The method can additionally be used to monitor of cellular immunity and cancer immune therapy by detection of specific T-cell frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human leukocyte antigen) peptides of human origin used in an example from the invention

```
Query Match      84.5%; Score 49; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 5
AAY69925
ID AAY69925 standard; peptide: 11 AA.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.
PT

Query Match 77.6%; Score 45; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
AAR47787
ID AAR47787 standard; protein; 14 AA.

Query Match 58.6%; Score 34; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5
 |||||
 DB 7 HYGP 11

RESULT 7
 AAR95759
 ID AAR95759 standard; peptide; 8 AA.
 XX AC
 XX AAR95759;
 XX
 DT 04-DEC-1996 (first entry)
 XX
 DE Alpha-4Beta-1 integrin binding inhibitory peptide 56.
 XX
 KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
 KW inhibitor; binding; white blood cell; migration; capillary wall;
 KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
 KW CSI; CS5; HI; LDV; active site.
 XX
 OS Synthetic.
 XX
 XX
 XX Key Location/Qualifiers
 FH Modified-site 8
 FT /note= "Pro-NH2"
 XX
 XX US5510332-A.
 XX
 XX 23-APR-1996.
 XX
 XX 07-JUL-1994; 94US-00271830.
 XX
 XX 07-JUL-1994; 94US-00271830.
 XX
 XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 XX
 XX Beck PV, Vanderslice P, Kogan TP, Ren K;
 XX WPI; 1996-221274/22.
 XX
 XX New peptide(s) based on the LDV domain of fibronectin - used for
 PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or
 PT invasive.
 XX
 XX Claim 4; Col 43-44; 35pp; English.
 XX
 XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
 XX surface of endothelial cells that line the interior wall of capillaries.
 XX VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or VLA-
 XX 4 for very late antigen-4), a heterodimeric protein present on the
 XX surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
 XX white blood cells to adhere to the capillary wall in areas where the
 XX tissue surrounding the capillary has been infected or damaged. Sometimes
 XX this white blood cell migration can become uncontrolled, with white blood
 XX cells flooding to the scene, causing widespread tissue damage. Cpds.
 XX capable of blocking this process may be beneficial as therapeutic agents.
 XX IA4B1 also recognises the extracellular matrix glycoprotein fibronectin.
 XX Three distinct IA4B1-binding sites have been identified within
 XX fibronectin. One site is found in the HepII region and is expressed in
 XX all isoforms; two others (CS1 and CS5) are present in the alternatively
 XX spliced type III connecting segments. CS1 has the higher affinity for
 XX IA4B1 and contains the tripeptide LDV as its minimal active site.
 XX Peptides AAR95704-805 are modeled after a portion of the CS1 peptide that
 XX include the LDV domain presented in such a way by its novel flanking
 XX sequence to produce a potent inhibitor of IA4B1 binding.
 XX
 XX Sequence 8 AA;
 SQ

Query Match 55.2%; Score 32; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5
 |||||
 DB 7 HYGP 11

RESULT 7
 AAR95759
 ID AAR95759 standard; peptide; 8 AA.
 XX AC
 XX AAR95759;
 XX
 DT 04-DEC-1996 (first entry)
 XX
 DE Alpha-4Beta-1 integrin binding inhibitory peptide 56.
 XX
 KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
 KW inhibitor; binding; white blood cell; migration; capillary wall;
 KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
 KW CSI; CS5; HI; LDV; active site.
 XX
 OS Synthetic.
 XX
 XX
 XX Key Location/Qualifiers
 FH Modified-site 8
 FT /note= "Pro-NH2"
 XX
 XX US5510332-A.
 XX
 XX 23-APR-1996.
 XX
 XX 07-JUL-1994; 94US-00271830.
 XX
 XX 07-JUL-1994; 94US-00271830.
 XX
 XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 XX
 XX Beck PV, Vanderslice P, Kogan TP, Ren K;
 XX WPI; 1996-221274/22.
 XX
 XX New peptide(s) based on the LDV domain of fibronectin - used for
 PT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1, fibronectin or
 PT invasive.
 XX
 XX Claim 4; Col 43-44; 35pp; English.
 XX
 XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
 XX surface of endothelial cells that line the interior wall of capillaries.
 XX VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or VLA-
 XX 4 for very late antigen-4), a heterodimeric protein present on the
 XX surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
 XX white blood cells to adhere to the capillary wall in areas where the
 XX tissue surrounding the capillary has been infected or damaged. Sometimes
 XX this white blood cell migration can become uncontrolled, with white blood
 XX cells flooding to the scene, causing widespread tissue damage. Cpds.
 XX capable of blocking this process may be beneficial as therapeutic agents.
 XX IA4B1 also recognises the extracellular matrix glycoprotein fibronectin.
 XX Three distinct IA4B1-binding sites have been identified within
 XX fibronectin. One site is found in the HepII region and is expressed in
 XX all isoforms; two others (CS1 and CS5) are present in the alternatively
 XX spliced type III connecting segments. CS1 has the higher affinity for
 XX IA4B1 and contains the tripeptide LDV as its minimal active site.
 XX Peptides AAR95704-805 are modeled after a portion of the CS1 peptide that
 XX include the LDV domain presented in such a way by its novel flanking
 XX sequence to produce a potent inhibitor of IA4B1 binding.
 XX
 XX Sequence 8 AA;
 SQ

Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWVM 9
 |||||
 DB 1 GPGWLDV 7

RESULT 8
 AAR88101
 ID AAR88101 standard; peptide; 8 AA.
 XX AC
 XX AAR88101;
 XX
 DT 22-JUL-1996 (first entry)
 XX
 DE Bovine p32 11-cis-retinol dehydrogenase tryptic fragment P322.
 XX
 KW Clone p-lambda-321; bovine; p32; 11-cis-retinol; dehydrogenase;
 KW 11-cis-retinaldehyde; diagnosis; psoriasis; acne and certain cancers (i.e. T-cell leukaemias),
 KW psoriasis; acne; cancer; T-cell leukaemia; drug development; treatment;
 KW retinal pigment epithelial cell; tryptic fragment; leukemia.
 XX
 OS Synthetic.
 XX
 XX WO9534580-A1.
 XX
 XX 21-DEC-1995.
 XX
 XX 06-JUN-1995; 95WO-US006256.
 XX
 XX 10-JUN-1994; 94US-00258418.
 XX
 XX 20-JAN-1995; 95US-00375962.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Hellman U, Wernstedt C, Eriksson U;
 XX WPI; 1996-049624/05.
 XX
 XX Nucleic acid encoding a retinol dehydrogenase protein - used to develop
 PT prods. for the diagnosis and treatment of retinoid-linked pathological
 PT conditions.
 XX
 XX Example 4; Page 10; 35pp; English.
 XX
 XX Bovine p32 11-cis-retinol dehydrogenase, which catalyses the conversion
 CC of 11-cis-retinol into 11-cis-retinaldehyde, can be used for the
 CC diagnosis of retinoid linked pathological conditions, e.g. retinitis
 CC pigmentosa, psoriasis, acne and certain cancers (i.e. T-cell leukaemias),
 CC and for the development of drugs to treat these conditions. The p32 DNA
 CC clone p-lambda-321 was isolated from bovine retinal pigment epithelial
 CC (RPE) cell mRNA, using degenerate primers based on the 32 kD bovine RPE
 CC cell derived protein p32 tryptic fragments AAR88100-04
 XX
 XX Sequence 8 AA;
 SQ

Query Match 53.4%; Score 31; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YGPGW 6
 |||||
 DB 1 YSPGW 5

RESULT 9
 AAW18339
 ID AAW18339 standard; peptide; 8 AA.
 XX AC
 XX AAW18339;
 XX
 XX 18-AUG-1997 (first entry)
 DT

XX DE Bovine p32 11-cis-retinol dehydrogenase tryptic peptide p322.
 XX KW 11-Cis retinol dehydrogenase; p32; 11-cis retinaldehyde;
 XX KW retinitis pigmentosa; psoriasis; acne; cancer; diagnosis; therapy.
 OS Bos taurus.
 XX PN WO9719167-A1.
 XX PD 29-MAY-1997.
 XX PF 14-NOV-1996; 96WO-US018295.
 XX PR 22-NOV-1995; 95US-00562114.
 XX PR 11-OCT-1996; 96US-00729594.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Eriksson U, Simon A, Romert A;
 XX WPI; 1997-298106/27.
 XX New 11-cis retinol dehydrogenase gene - used to develop products for the
 PT diagnosis and therapy of conditions such as retinitis pigmentosa,
 PT psoriasis and cancers.
 XX PS Example 4; Page 11; 68pp; English.
 XX CC Tryptic peptides (AAW18338-42) were isolated from bovine retinal pigment
 CC epithelial (RPE) membrane protein p32. PCR primers (see also AAT68946-49)
 CC based on these primers were used to amplify cDNA (see also AAT68935)
 CC coding for bovine p32 (AAW18443) from a RPE cDNA library. Peptide p322
 CC corresponds to amino acids 281-288 of the p32 sequence deduced from the
 CC cDNA clone. p32 is an 11-cis retinol dehydrogenase and forms a complex
 CC with a component of the membrane receptor for retinol binding protein
 XX SQ Sequence 8 AA;
 Query Match 53.4%; Score 31; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YGPGW 6
 DB 1 YSPGW 5
 RESULT 10
 AAY01930
 ID AAY01990 standard; peptide; 8 AA.
 AC AAY01990;
 XX 02-JUL-1999 (first entry)
 XX DT
 XX DE Tryptic peptide of bovine p32 protein.
 XX KW p32 protein; retinol dehydrogenase; 9-cis; 11-cis; 13-cis;
 KW trans retinol dehydrogenase; oligomeric protein complex;
 KW membrane receptor; retinol binding protein;
 KW short chain alcohol dehydrogenase family; retinaldehyde;
 KW retinitis pigmentosa; skin disorder; psoriasis; acne; T-cell leukemia.
 XX Bcs sp.
 XX PN WO9916788-A1.
 XX PD 08-APR-1999.
 XX 21-SEP-1998; 98WO-US019836.
 XX 26-SEP-1997; 97US-00937993.

XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Eriksson U, Simon A, Romert A;
 XX DR WPI; 1999-255059/21.
 XX PT New retinol dehydrogenase proteins, used to screen potential retinoid
 PT drugs for treatment of various diseases, e.g. retinitis pigmentosa.
 XX PS Example 4; Page 14; 88pp; English.
 XX CC AAY01989-93 represent peptide obtained after tryptic digest of a p32
 CC protein, isolated in the course of the invention. The specification
 CC describes proteins having retinol dehydrogenase activity, such as 9-cis,
 CC 11-cis, 13-cis, or trans retinol dehydrogenase activity. These proteins
 CC form oligomeric protein complexes with the components of the membrane
 CC receptor for retinol binding protein. The retinol dehydrogenase proteins
 CC are members of the short chain alcohol dehydrogenase family. The
 CC recombinant enzymes can be used to produce 9-cis and 11-cis
 CC retinaldehydes. The proteins and nucleic acids encoding them can be used
 CC to screen potential retinoid drugs for treatment of various diseases,
 CC e.g. diseases of the eye such as retinitis pigmentosa and skin disorders
 CC such as psoriasis and acne. Certain T-cell leukemias may also be tested
 CC by retinoid drugs. Antibodies against the protein can be used to monitor
 CC pathological conditions characterized by aberrant levels of a receptor
 CC for retinol binding protein
 XX SQ Sequence 8 AA;
 Query Match 53.4%; Score 31; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YGPGW 6
 DB 1 YSPGW 5
 RESULT 11
 ABP46859
 ID ABP46859 standard; peptide; 8 AA.
 AC ABP46859;
 XX 19-AUG-2002 (first entry)
 XX DT
 XX DE Human BlyS binding scFv VH CDR3 SEQ ID 2870.
 KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antineumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX PN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX 15-JUN-2001; 2001WO-US019110.
 XX 16-JUN-2000; 2000US-0212210P.
 XX 17-OCT-2000; 2000US-0240816P.
 XX 16-MAR-2001; 2001US-0276248P.
 XX 21-MAR-2001; 2001US-0277379P.
 XX 23-MAY-2001; 2001US-0293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 2; Page 3068; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumor necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 51.7%; Score 30; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GPGW 6
 Db |||||
 2 GPGW 5
 RESULT 12
 AAP95363
 ID AAP95363 standard; peptide; 9 AA.
 XX
 AC AAP95363;
 XX
 XX 30-MAR-1992 (first entry)
 DT
 XX
 XX Variable region V3, found in the envelope protein gp120 of an AIDS or ARC
 DE causing or related virus strain MAL.
 DE
 XX Vaccine; AIDS; ARC; HIV; diagnosis.
 KW
 XX AIDS virus.
 OS
 XX EP311219-A.
 PN
 XX 12-APR-1989.
 PD
 XX 07-OCT-1988; 88EP-00202248.
 XX
 XX 09-OCT-1987; 87NL-00002403.
 XX
 XX (DIER-) STICHTING CENT DIER.
 PA (UNAM) UNIV VAN AMSTERDAM.
 PA (UYAM-) UNIV AMSTERDAM ZIEKENHUI.
 XX
 XX Goudsmit J, Melen RH;
 PI
 XX WPI; 1989-108193/15.
 DR
 XX Oligopeptide(s) corresp. to beta-turn variable region of gp.120 - used
 XX for diagnosis of and prodn of vaccines against AIDS and ARC.
 PT
 XX Disclosure; Page 4; 7pp; English.
 XX

XX The peptides of the invention comprise the beta-turn AA SQ GPG or GPGR at
 CC positions 312-314 or 312-315 in the AA numbering of HTLV-IIIB (BH10) and
 CC flanking AA SQs having a length equal to or greater than 1 and pref.
 CC equal to or greater than 2 AAs; variants in which the GPG or GPGR SQ has
 CC been replaced by a different beta-turn SQ; and variants in which the free
 CC NH₂-terminal gp AA and/or the free carboxyl terminal gp. AA has been
 CC blocked or modified otherwise
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 51.7%; Score 30; DB 1; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HVGPG 5
 Db |||||
 2 HVGPG 6
 RESULT 13
 AAR31288
 ID AAR31288 standard; peptide; 9 AA.
 XX
 AC AAR31288;
 XX
 XX 12-FEB-1993 (first entry)
 DT
 XX HIV principal determinant peptide.
 DE
 XX AIDS; ARC; human immunodeficiency virus; vaccine; Neisseria;
 KW meningitidis b; outer membrane protein complex; OMPC; PND-MAL.
 KW
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "bonds to the OMPC of the conjugate via this site"
 XX
 XX EP467700-A.
 PN
 XX 22-JAN-1992.
 PD
 XX 19-JUL-1991; 91EP-00306598.
 XX
 XX 19-JUL-1990; 90US-00555339.
 PR 19-JUL-1990; 90US-00555366.
 PR 19-JUN-1991; 91US-00715276.
 PR 19-JUN-1991; 91US-00715278.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 XX
 PI Leanza WJ, Marburg S, Tolman RL, Emini EA;
 XX
 XX WPI; 1992-026505/04.
 DR
 XX Conjugate proteins comprising HIV peptide components - useful for
 PT preparing vaccines for e.g. AIDS or for treating infections.
 XX
 XX Claim 12; Page 56; 63pp; English.
 XX
 XX The invention relates to a co-conjugate comprising an immunogenic protein
 CC or protein complex having a first set of covalent linkages to low
 CC molecular weight moieties which have an anionic or polyanionic character
 CC at physiological pH, and a second set of covalent linkages to peptides
 CC comprising HIV principal neutralizing determinants (PND's) or
 CC immunologically equivalent peptides. Preferably at least one set of the
 CC covalent linkages is comprised of maleimide derivatives; the
 CC (poly)anionic moiety is composed of one to five residues of the anionic
 CC form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
 CC protein is the outer membrane protein complex (OMPC) of Neisseria
 CC meningitidis b; and the PND peptide has a linear structure, a disulphide-
 CC bonded cyclic structure, an amide-bonded cyclic structure or a thioether-

CC bonded cyclic structure. The present sequence (PND-MAL) is an example of
 CC a PND peptide component used in the co-conjugate. The co-conjugate is
 CC useful for inducing anti-peptide immune response in mammals, for inducing
 CC HIV-neutralizing antibodies in mammals, for formulating vaccines to
 CC prevent HIV infection or disease, including AIDS, or for treating humans
 CC afflicted with HIV infection or disease

XX Sequence 9 AA;

Query Match 51.7%; Score 30; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
 | : | | |
 Db 2 HFGPG 6

RESULT 14

AAR30043
 ID AAR30043 standard; peptide; 9 AA.

XX AC AAR30043;

XX AC AAR30043;

DT 25-MAR-2003 (revised)

DT 28-APR-1993 (first entry)

XX HIV principle neutralising determinant MAL.

XX Human immunodeficiency virus; AIDS; PND; MIEP; conjugate;
 KW major immune enhancing protein; vaccine; anti-HIV antibodies; immunogen;
 KW passive immunisation.

XX Human immunodeficiency virus.

XX EP519554-A1.

XX 23-DEC-1992.

XX 11-JUN-1992; 92EP-00201693.

XX 19-JUN-1991; 91US-00715273.

XX (MERI) MERCK & CO INC.

XX Emini A, Liu MA, Marburg S, Tolman RL;

XX WPI; 1992-425771/52.

XX Conjugates of HIV-1 PND peptide(s) with the MIEP of Neisseria
 PT meningitidis - useful as a vaccine for treating and preventing HIV-1
 PT infection, e.g. AIDS in humans.

XX Claim 9; Page 60; 66pp; English.

XX The peptide is HIV principle neutralising determinant (PND) MAL and is
 CC used as part of a conjugate comprising the major immune enhancing protein
 CC (MIEP) of Neisseria meningitidis covalently linked to the HIV PND. The
 CC conjugate may be used to prepare vaccines against HIV infections, e.g.
 CC AIDS, as research tools for studying PND structure- function
 CC relationships, or as immunogens for use in the passive immunisation of
 CC humans. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 51.7%; Score 30; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
 | : | | |
 Db 2 HFGPG 6

RESULT 15

AAR26724
 ID AAR26724 standard; peptide; 9 AA.

XX AC AAR26724;

XX 09-FEB-1993 (first entry)

XX HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;
 KW outer membrane protein complex; OMPC; Neisseria; AIDS; PND-MAL.

XX Synthetic.

XX Key

Location/Qualifiers

Modified-site 1

FT /note= "Joins onto polysaccharide-protein complex via
 FT this site"

XX EP468714-A.

XX 29-JAN-1992.

XX 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555574.

XX 19-JUN-1991; 91US-00715275.

XX 19-JUN-1991; 91US-00715277.

XX (MERI) MERCK & CO INC.

XX Marburg S, Tolman RL, Emini EA;

XX WPI; 1992-034437/05.

XX HIV peptide-polysaccharide-protein conjugates - used in vaccines or to
 PT produce antibodies to prevent or treat HIV infection.

XX Claim 9; Page 57; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing
 CC determinant (PND), or an immunologically equivalent peptide (PEP),
 CC covalently coupled to an immunogenic protein or protein complex through
 CC an anionic polysaccharide linker. Pref. the immunogenic protein is the
 CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the
 CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,
 CC an anide-bonded cyclic structure or a thioether-bonded cyclic structure.
 CC The present sequence (PND-MAL) is an example of a PND peptide component.
 CC The conjugates are used for inducing HIV-neutralising antibodies or for
 CC making vaccines to prevent contraction of HIV infection or disease. The
 CC antibodies can be used for passively protecting against infection by HIV,
 CC or for protecting against proliferation of HIV post-infection, or for
 CC treating AIDS, or in diagnostic assays

XX Sequence 9 AA;

Query Match 51.7%; Score 30; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGPG 5
 | : | | |
 Db 2 HFGPG 6

RESULT 16

AAU98826
 ID AAU98826 standard; peptide; 11 AA.

XX AAU98826;

XX DT 22-AUG-2002 (first entry)
 XX DE Adenovirus targeting peptide #6.
 XX KW Targeting peptide; cancer; adenovirus targeting; cytostatic; anti-HIV;
 XX KW immunostimulant; immunogen; cancer; human immunodeficiency virus; HIV;
 XX KW vector delivery.
 XX OS Synthetic.
 XX FN WO200220724-A2.
 XX PD 14-MAR-2002.
 XX PF 07-SEP-2001; 2001WO-US028045.
 XX FR 08-SEP-2000; 2000US-0231266P.
 XX FR 17-JAN-2001; 2001US-00765101.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Arap W, Pasqualini R;
 XX DR WPI; 2002-489672/52.
 XX PT Modulation of immune system response comprises administration of
 XX PT targeting peptide attached to immunogen.
 XX PS Claim 22; Page 51; 86pp; English.
 XX CC This invention relates to a method for modulating the immune system
 CC response comprising administration of a lymph node targeting peptide
 CC attached to an immunogen. The invention also comprises a bispecific
 CC compound comprising the sequences Cys-Ala-Tyr or Ser-Cys-Ala-Arg, a
 CC bispecific compound comprising a targeting peptide attached to a vector
 CC binding moiety and a method for targeting a vector to an organ or tissue
 CC comprising administering the vector and a complex comprising a targeting
 CC peptide and a binding moiety. The peptides of the invention may have
 CC cytostatic, anti-HIV or immunostimulant activities. The method of the
 CC invention is useful for increasing the immune response to an immunogen,
 CC especially a cancer cell or human immunodeficiency virus (HIV). The
 CC method is useful for the selective delivery of gene therapy vectors. The
 CC present sequence represents an adenovirus homing peptide used in the
 CC method of the invention
 XX SQ Sequence 11 AA;
 Query Match 51.7%; Score 30; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GPGW 6
 ||||
 DB 8 GPGW 11
 RESULT 17
 AAU83484
 ID AAU83484 standard; peptide; 12 AA.
 XX AC AAU83484;
 XX DT 08-MAY-2002 (first entry)
 XX DE PPV V1up PLA2-binding peptide p6.
 XX KW Phospholipase A2; enzyme; PLA2; virucide; antirheumatic; antiarthritic;
 XX KW immunosuppressive; parvovirus; V1up; gene therapy;
 XX KW viral-associated disease; rheumatoid arthritis; systemic erythematosis;
 XX KW adult-onset Still's disease; polyarthritis; phage display.
 XX OS Unidentified.

XX WO200200924-A2.
 XX PD 03-JAN-2002.
 XX PF 28-JUN-2001; 2001WO-CA000932.
 XX PR 28-JUN-2000; 2000CA-02310263.
 XX PA (NARE-) INST NAT RECH SCI.
 XX TI Tijssen P, Zadori Z;
 XX PI WPI; 2002-139932/18.
 XX DR N-PSDB; ABK33266.
 XX PT New viral phospholipase A2 enzymes, useful in gene therapy for treating a
 XX PT subject viral-associated disease, e.g. rheumatoid arthritis, systemic
 XX PT erythematosis, adult-onset Still's disease or polyarthritis.
 XX PS Example 10; Fig 13; 107pp; English.
 XX CC The invention relates to an isolated viral polypeptide having
 CC phospholipase A2 (PLA2) activity (e.g. V1up from parvoviruses) and the
 CC polynucleotides encoding them. Also included are a peptide that
 CC specifically binds a viral phospholipase A2 being (WV)-(CIVL)-G-x-(GP)-
 CC (GKNS)-x(8,14)-D-x(2)-(AC)-x(2)-x(2)-H-D-x(2)-Y. () = indicates the
 CC presence of one of the enclosed amino acids at this position; x = any
 CC amino acid; x(2) = a stretch of 2 amino acids; and x(8,14) = a stretch of
 CC 8-14 amino acids or Y-X-G-P-G-x(12)-D-x(2)-A-x(2)-H-D-x(2)-Y, a
 CC polypeptide that is an inactive variant of a viral polypeptide comprising
 CC an amino acid motif as detailed above, an antisense oligonucleotide
 CC complementary to the polynucleotide, a vector comprising the
 CC polynucleotide, a host cell comprising the vector, producing a
 CC recombinant virus comprising genetically engineered viral particles with
 CC the polynucleotide, fragment or vector, an antibody that bind to the
 CC protein, anti viral compounds which inhibit viral phospholipases. The
 CC polynucleotide is useful for gene therapy, and for improving a gene-
 CC therapy vector, where the gene therapy vector is based on an adeno-
 CC associated virus. The antisense oligonucleotide is useful for inhibiting
 CC viral replication and/or infectivity in a subject, for manufacturing a
 CC medicament to decrease the infectivity and/or replication of a virus in a
 CC subject or to treat viral-associated disease. The polypeptide is useful
 CC as an in vitro standard for measuring phospholipase A2 activity. The anti
 CC -viral agent is used to decrease the infectivity and/or replication of a
 CC virus, e.g. parvovirus, in a subject. The anti-viral agent may also used
 CC to inhibit a viral phospholipase A2 in a subject in need of such therapy,
 CC where the subject has a viral-associated disease or disorder,
 CC particularly a disease associated with a parvovirus. The viral-associated
 CC disease includes rheumatoid arthritis, systemic erythematosis, adult-
 CC onset Still's disease or polyarthritis. The present sequence is a phage
 CC -displayed peptide which binds Parvovirus V1up peptide
 XX SQ Sequence 12 AA;
 Query Match 51.7%; Score 30; DB 5; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 HYGPGWVS 8
 ||||
 DB 5 HYPHPWTA 12
 RESULT 18
 AAR47733
 ID AAR47733 standard; protein; 13 AA.
 XX AC AAR47733;
 XX DT 25-MAR-2003 (revised)
 XX DT 27-JUL-1994 (first entry)
 XX

DE HIV epitope #66.
 XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.
 XX Human immunodeficiency virus.
 OS
 XX WO9402626-A1.
 XX
 XX 03-FEB-1994.
 XX
 XX 19-JUL-1993; 93WO-US006751.
 XX
 XX 20-JUL-1992; 92US-00917212.
 PR 20-JUL-1992; 92US-00917214.
 PR 20-JUL-1992; 92US-00917215.
 PR 20-JUL-1992; 92US-00917217.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Keller PM, Conley AJ, Shaw AR, Arnold BA;
 XX WPI; 1994-048884/06.
 XX
 XX New conjugates for treating or preventing HIV infection - comprising HIV-specific neutralisation epitopes covalently linked to outer membrane proteosome of Neisseria.
 PT
 PT
 XX Claim 1; Page 124; 181pp; English.
 XX
 XX The sequences given in AAR47668-788 are HIV-specific selected principal neutralisation epitopes which may be used in an antigenic conjugate linked to purified outer membrane proteosome of Neisseria. This conjugate may be used in an AIDS vaccine which may be used pre- and post-exposure to prevent or treat HIV infection or disease. The vaccine is capable of eliciting specific HIV neutralising antibodies and bind the broadly neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR -2003 to correct PN field.)
 CC
 CC
 XX Sequence 13 AA;
 SQ
 Query Match 51.7%; Score 30; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGP 5
 Db 4 HFGPG 8
 RESULT 19
 AAR47760
 ID AAR47760 standard; protein; 14 AA.
 XX
 XX AAR47760;
 AC
 XX 25-MAR-2003 (revised)
 DT 27-JUL-1994 (first entry)
 XX
 XX HIV epitope #93.
 DE
 XX
 XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.
 XX
 XX Human immunodeficiency virus.
 OS
 XX WO9402626-A1.
 XX
 XX 03-FEB-1994.
 XX
 XX 19-JUL-1993; 93WO-US006751.
 PF

XX 20-JUL-1992; 92US-00917212.
 PR 20-JUL-1992; 92US-00917214.
 PR 20-JUL-1992; 92US-00917215.
 PR 20-JUL-1992; 92US-00917217.
 XX
 XX (MERI) MERCK & CO INC.
 XX
 XX Keller PM, Conley AJ, Shaw AR, Arnold BA;
 XX WPI; 1994-048884/06.
 XX
 XX New conjugates for treating or preventing HIV infection - comprising HIV-specific neutralisation epitopes covalently linked to outer membrane proteosome of Neisseria.
 PT
 PT
 XX Claim 1; Page 138; 181pp; English.
 XX
 XX The sequences given in AAR47668-788 are HIV-specific selected principal neutralisation epitopes which may be used in an antigenic conjugate linked to purified outer membrane proteosome of Neisseria. This conjugate may be used in an AIDS vaccine which may be used pre- and post-exposure to prevent or treat HIV infection or disease. The vaccine is capable of eliciting specific HIV neutralising antibodies and bind the broadly neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR -2003 to correct PN field.)
 CC
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 51.7%; Score 30; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGP 5
 Db 4 HFGPG 8
 RESULT 20
 ADD94624
 ID ADD94624 standard; peptide; 10 AA.
 XX
 XX ADD94624;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Human SIMP-derived peptide 144.
 DE
 XX
 XX source of immunodominant MHC-associated peptide; SIMP; MHC;
 KW major histocompatibility complex; human leukocyte antigen; HLA;
 KW cytostatic; immunosuppressive; antineoplastic therapy; gene therapy; cancer;
 KW lung cancer; intestine cancer; sarcoma; prostate cancer;
 KW testicular cancer; breast cancer; melanomas; pancreatic cancer;
 KW haematological cancer; immune response; lymphoid cell proliferation;
 KW autoimmune disease; transplant rejection; SIMP-derived peptide; human.
 XX
 XX Homo sapiens.
 OS
 XX WO2003054008-A2.
 XX
 XX 03-JUL-2003.
 PD
 XX
 XX 18-DEC-2002; 2002WO-CA001967.
 PF
 XX 20-DEC-2001; 2001US-00028384.
 PR
 XX (COMP-) COMPATIGENE INC.
 PA
 XX Perreault C, McBride K;
 PI
 XX WPI; 2003-559122/52.
 DR
 XX New human source of immunodominant MHC-associated peptide (SIMP) nucleic
 PT

PT acids and proteins, useful for diagnosing and treating cancers, e.g. lung
 PT or breast cancer, or for suppressing an immune response in an autoimmune
 PT disease.

PS Claim 24; Page 19; 66pp; English.

XX This invention relates to a novel isolated or purified human protein,
 XX termed source of immunodominant major histocompatibility complex (MHC) -
 CC associated peptide (SIMP), which is expressed ubiquitously in human
 CC cells, where the protein has the potential of generating several protein
 CC fragments binding with high affinity to a human leukocyte antigen (HLA)
 CC molecule. The invention may allow development of therapeutics with
 CC cytostatic or immunosuppressive activity or provide sequences useful for
 CC antisense therapy or gene therapy. The source of immunodominant MHC-
 CC associated peptide (SIMP) nucleic acids, proteins and fragments are
 CC useful for diagnosing and treating cancers, for example lung cancer,
 CC intestine cancer, sarcomas, prostate cancer, testicular cancer, breast
 CC cancer, melanomas, pancreatic cancer or hematological cancer. The SIMP
 CC proteins are also useful for modulating an immune response. Decreasing
 CC lymphoid cell proliferation is useful for suppressing an immune response
 CC responsible for an autoimmune disease or a transplant rejection. The
 CC present sequence is that of a human SIMP-derived peptide (with a high
 CC affinity binding motif for HLA molecules) of the invention.

XX Sequence 10 AA;

Query Match 50.0%; Score 29; DB 7; Length 10;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYPGG 5
 |:|
 Db 5 HHGPG 9

RESULT 21

AAAR47732
 ID AAR47732 standard; protein; 14 AA.

XX AAR47732;

25-MAR-2003 (revised)
 27-JUL-1994 (first entry)

XX HIV epitope #65.

KW HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.

OS Human immunodeficiency virus.

XX WO9402626-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006751.

XX 20-JUL-1992; 92US-00917212.

XX 20-JUL-1992; 92US-00917214.

XX 20-JUL-1992; 92US-00917215.

XX 20-JUL-1992; 92US-00917217.

XX (MERI) MERCK & CO INC.

XX Keller PM, Conley AJ, Shaw AR, Arnold BA;

XX WPI; 1994-048884/06.

XX New conjugates for treating or preventing HIV infection - comprising HIV-

XX specific neutralisation epitopes covalently linked to outer membrane

XX proteosome of Neisseria.

PS Claim 1; Page 124; 181pp; English.

XX The sequences given in AAR47668-788 are HIV-specific selected principal
 CC neutralisation epitopes which may be used in an antigenic conjugate
 CC linked to purified outer membrane proteosome of Neisseria. This conjugate
 CC may be used in an AIDS vaccine which may be used pre- and post-exposure
 CC to prevent or treat HIV infection or disease. The vaccine is capable of
 CC eliciting specific HIV neutralising antibodies and bind the broadly
 CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
 CC -2003 to correct PN field.)

XX Sequence 14 AA;

Query Match 50.0%; Score 29; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYPGG 5
 |:|
 Db 4 HHGPG 8

RESULT 22

AAAM98717

ID AAM98717 standard; peptide; 14 AA.

XX AC AAM98717;

XX 24-JAN-2002 (first entry)

XX Human peptide #1992 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 99US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.

XX Disclosure; Page 4105; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX
 SQ Sequence 14 AA;
 Query Match 50.0%; Score 29; DB 4; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GPGWVS 8
 DB 8 GPWWIS 13
 RESULT 23
 ABB45010
 ID ABB45010 standard; peptide; 8 AA.
 XX
 AC ABB45010;
 XX
 DT 06-FEB-2002 (first entry)
 XX
 DE Human albumin-binding peptide #59.
 XX
 KW Peptide ligand; immunoglobulin G; IgG; serum albumin; human.
 XX
 OS Synthetic.
 XX
 PN WO200145746-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000WO-US035325.
 XX
 PR 23-DEC-1999; 99US-0173048P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Delano WL, Dennis MS, Lowman HB;
 XX
 DR WPI; 2001-514266/56.
 XX
 PT Peptide ligands with affinity for immunoglobulin (Ig) G, IGM and/or human
 PT serum albumin which may be conjugated to, and used to prolong the
 PT elimination half-time of active agents from the circulation.
 XX
 PS Example 6; Fig 5; 71pp; English.
 XX
 CC The present invention relates to novel peptide ligands with affinity for
 CC immunoglobulin (Ig) G or serum albumin. The peptide ligands may be
 CC conjugated to, and used to prolong the elimination half-time of,
 CC therapeutic and diagnostic agents in the body. The present sequence is a
 CC human albumin-binding peptide used to illustrate the invention
 XX
 SQ Sequence 8 AA;
 Query Match 48.3%; Score 28; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PGWV 7
 DB 4 PGWV 7
 RESULT 24
 AAR76078
 ID AAR76078 standard; peptide; 10 AA.

XX
 AC AAR76078;
 XX
 DT 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 XX
 DE Phage display peptide.
 XX
 KW Antigen binding structure; complementarity determining region; CDR;
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
 KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
 KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin; phage M13; phage display.
 XX
 OS Synthetic.
 XX
 PN WO9515382-A1.
 XX
 PD 08-JUN-1995.
 XX
 PF 29-NOV-1994; 94WO-GB002610.
 XX
 PR 03-DEC-1993; 93GB-00024819.
 PR 03-JUN-1994; 94GB-00011089.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
 PI Blakey DC;
 XX
 DR WPI; 1995-215262/28.
 XX
 PT Antigen binding structures containing CDR's recognising the CA55.1
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis
 PT and therapy of cancer.
 XX
 PS Claim 1; Page 96; 121pp; English.
 XX
 CC An antigen binding structure (I) is based on the CDRs (given in AAR76078-
 CC 84) of the heavy and light chains of Mab 55.1 (ECACC 93081901), which
 CC recognises the colorectal tumor-associated antigen CA55.1. The peptide
 CC given in AAR76078, as displayed on the surface of phage NCIMB 40638,
 CC binds to (I) with an effective binding of 10 pM or less, and
 CC competitively inhibits binding of (I) to Colo 205 cells (ATCC CCL 222).
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 Query Match 48.3%; Score 28; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGEGW 6
 DB 4 HRGSGW 9
 RESULT 25
 AAY31073
 ID AAY31073 standard; peptide; 10 AA.
 XX
 AC AAY31073;
 XX
 DT 21-OCT-1999 (first entry)
 XX
 DE Non-crosslinked protein particle peptide 122.
 XX
 KW Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; nanometer; micrometer; clearance.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

XX 13-NOV-1995; 95US-00556597.
 PR (UUNY) UNIV NEW YORK STATE RES FOUND.
 PA Miller JL, Lyle VA;
 XX WPI; 1997-289227/26.
 XX Peptide which mimics human platelet glycoprotein Ib/IX complex epitope -
 PT also anti-mimotope molecule capable of binding to the peptide and useful
 PT to modulate platelet adhesion, aggregation or agglutination.
 XX Claim 3; Page 97; 115pp; English.
 XX The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits the
 CC ristocetin induced aggregation of platelets
 XX Sequence 12 AA;
 SQ

Query Match 48.3%; Score 28; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YGPGWV 7
 DB :|||
 3 FGPFVW 8

RESULT 28
 AAW71785
 ID AAW71785 standard; peptide; 12 AA.
 AC AAW71785;
 XX 08-DEC-1998 (first entry)
 DT Mimotope capable of binding to monoclonal antibody C-34 #33.
 DE Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 XX binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 XX Synthetic.
 OS Homo sapiens.
 XX US5817748-A.
 PN 06-OCT-1998.
 PD 17-MAR-1995; 95US-00406330.
 XX 17-MAR-1995; 95US-00406330.
 PR (UUNY) UNIV NEW YORK STATE RES FOUND.
 XX Miller JL, Lyle VA;
 PI WPI; 1998-556458/47.
 XX Peptides that mimic platelet epitope - and neutralise aggregation-
 PT inhibiting antibody.
 XX Disclosure; Col 5; 26pp; English.
 PS

XX The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides AAW71752 to AAW71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be an
 CC antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic drugs.
 CC A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets through
 CC the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes
 XX Sequence 12 AA;
 SQ

Query Match 48.3%; Score 28; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 YGPGWV 7
 DB :|||
 3 FGPFVW 8

RESULT 29
 AAE27766
 ID AAE27766 standard; peptide; 13 AA.
 XX AAE27766;
 XX 13-DEC-2002 (first entry)
 DT Human beta-glucocerebrosidase (beta-GCR) peptide #181.
 DE Human; fusion protein; immunological; major histocompatibility complex;
 KW MHC; gastric upset; beta-glucocerebrosidase; beta-GCR; enzyme;
 KW b-D-glucosyl-N-acylsphingosine glucosylase; E.C.3.2.1.45.
 XX Homo sapiens.
 OS WO200266514-A2.
 PN 29-AUG-2002.
 PD 18-FEB-2002; 2002WO-EP001690.
 XX 19-FEB-2001; 2001EP-00103955.
 PR 05-APR-2001; 2001EP-00108291.
 XX (MERE) MERCK PATENT GMBH.
 PA Gillies S, Carr FU, Jones T, Carter G, Hamilton A, Williams S;
 XX Hanlon M, Watkins J, Baker M, Way JC;
 PI WPI; 2002-667054/71.
 XX New modified fusion protein with reduced immunogenicity, useful for
 PT combining favorable properties of a composition, comprises an
 PT immunoglobulin molecule linked to a non-immunoglobulin target
 PT polypeptide.
 XX Example 10; Page 61; 92pp; English.
 PS The invention relates to an immunogenically modified fusion protein
 CC derived from a parent fusion protein, comprising first and second
 CC proteins/polypeptides, where the first protein is an immunoglobulin
 CC molecule or its fragment and the second protein is non-immunoglobulin
 CC target polypeptide each linked to the other directly or by a linker
 CC

CC molecule. The immunogenically modified fusion protein is useful in
 CC combining known favourable properties of a composition or in creating new
 CC properties of a composition which elicits biological or pharmacological
 CC efficacy without having undesirable physiological effects such as nausea
 CC or gastric upset. The present sequence is human beta-glucocerebrosidase
 CC (beta-GCR) peptide with potential major histocompatibility complex (MHC)
 CC binding activity. The beta-GCR peptide is also referred to as b-D-
 CC glucosyl-N-acetylphingosine glucosylase (B.C.3.2.1.45). This peptide is
 CC used in the exemplification of the invention
 XX
 SQ Sequence 13 AA;

Query Match 48.3%; Score 28; DB 5; Length 13;
 Best Local Similarity 80.0%; Pred. No. 5.2e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GPGWV 7
 ||||
 Db 8 GPNWV 12

RESULT 30
 AAR47734
 ID AAR47734 standard; protein; 14 AA.
 XX
 AC AAR47734;

XX
 XX 25-MAR-2003 (revised)
 DT 27-JUL-1994 (first entry)
 XX
 XX HIV epitope #67.

XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.
 XX
 OS Human immunodeficiency virus.

XX
 XX WO9402626-A1.
 XX
 XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006751.
 XX
 XX 20-JUL-1992; 92US-00917212.
 PR 20-JUL-1992; 92US-00917214.
 PR 20-JUL-1992; 92US-00917215.
 PR 20-JUL-1992; 92US-00917217.

XX (MERI) MERCK & CO INC.

XX Keller PM, Conley AJ, Shaw AR, Arnold BA;

XX WPI; 1994-048884/06.

XX New conjugates for treating or preventing HIV infection - comprising HIV-
 PT specific neutralisation epitopes covalently linked to outer membrane
 PT proteosome of Neisseria.

XX Claim 1; Page 125; 181pp; English.

XX The sequences given in AAR47668-788 are HIV-specific selected principal
 CC neutralisation epitopes which may be used in an antigenic conjugate
 CC linked to purified outer membrane proteosome of Neisseria. This conjugate
 CC may be used in an AIDS vaccine which may be used pre- and post-exposure
 CC to prevent or treat HIV infection or disease. The vaccine is capable of
 CC eliciting specific HIV neutralising antibodies and bind the broadly
 CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
 CC -2003 to correct PN field.)

XX Sequence 14 AA;

Query Match 48.3%; Score 28; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 4
 ||||
 Db 4 HYGP 7

RESULT 31
 AAR47770
 ID AAR47770 standard; protein; 14 AA.
 XX
 AC AAR47770;

XX 25-MAR-2003 (revised)
 DT 27-JUL-1994 (first entry)
 XX
 XX HIV epitope #103.

XX HIV-specific; principal neutralisation; epitope; antigen; conjugate;
 KW outer membrane proteosome; Neisseria; AIDS; vaccine; HIV; infection;
 KW disease; antibody; human; monoclonal antibody; 447 antibody.

XX Human immunodeficiency virus.

XX WO9402626-A1.

XX 03-FEB-1994.

XX 19-JUL-1993; 93WO-US006751.

XX 20-JUL-1992; 92US-00917212.

PR 20-JUL-1992; 92US-00917214.

PR 20-JUL-1992; 92US-00917215.

PR 20-JUL-1992; 92US-00917217.

XX (MERI) MERCK & CO INC.

XX Keller PM, Conley AJ, Shaw AR, Arnold BA;

XX WPI; 1994-048884/06.

XX New conjugates for treating or preventing HIV infection - comprising HIV-
 PT specific neutralisation epitopes covalently linked to outer membrane
 PT proteosome of Neisseria.

XX Claim 1; Page 143; 181pp; English.

XX The sequences given in AAR47668-788 are HIV-specific selected principal
 CC neutralisation epitopes which may be used in an antigenic conjugate
 CC linked to purified outer membrane proteosome of Neisseria. This conjugate
 CC may be used in an AIDS vaccine which may be used pre- and post-exposure
 CC to prevent or treat HIV infection or disease. The vaccine is capable of
 CC eliciting specific HIV neutralising antibodies and bind the broadly
 CC neutralising human monoclonal antibody (447 antibody). (Updated on 25-MAR
 CC -2003 to correct PN field.)

XX Sequence 14 AA;

Query Match 48.3%; Score 28; DB 2; Length 14;
 Best Local Similarity 80.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYGP 5
 :|||
 Db 4 YGPG 8

RESULT 32
 AAY57711
 ID AAY57711 standard; peptide; 14 AA.
 XX
 AC AAY57711;

XX DT 14-MAR-2000 (first entry)
 XX DE Rat clusterin 47 kDa peptide.
 XX KW Clusterin; immunosuppressant; organ rejection; tissue transplantation;
 XX KW autoimmune disease; inflammatory disease; rheumatism; atopy;
 XX KW systemic erythematosis; allergy; hay fever.
 XX OS Rattus sp.
 XX PN WO9962541-A1.
 XX PD 09-DEC-1999.
 XX PF 13-MAY-1999; 99WO-JP002474.
 XX PR 01-JUN-1998; 98JP-00151570.
 XX PA (HISM) HISAMITSU PHARM CO LTD.
 XX PI Yuda K, Akiyama K, Goto T, Goto S;
 XX WI 2000-072735/06.
 XX PT Immunosuppressants with reduced side-effects, useful for preventing
 PT rejection in organ and tissue transplant and as remedies for autoimmune
 PT diseases and inflammatory diseases (claimed) e.g. allergy.
 XX PS Example 3; Page 12; 28pp; Japanese.
 XX CC The present invention describes an immunosuppressant which contains a
 CC clusterin. The present sequence represents a rat clusterin peptide from
 CC an example of the present invention. Also described is a method for
 CC treating rejection in organ and tissue transplant, autoimmune diseases or
 CC inflammatory diseases by administering an effective dose of the
 CC immunosuppressant. The immunosuppressant are useful for preventing
 CC rejection in organ and tissue transplant, particularly of heart, liver,
 CC lung, pancreas, kidney, small intestine, skin and bone marrow, and as
 CC remedies for autoimmune diseases such as rheumatism, atopy, systemic
 CC erythematosis, and inflammatory diseases including allergy such as hay
 CC fever. The drugs are efficacious, with little side-effects
 XX SQ Sequence 14 AA;
 Query Match 48.3%; Score 28; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYGP 4
 DB 7 HYGP 10
 RESULT 33
 ABG66144
 ID ABG66144 standard; peptide; 13 AA.
 XX AC ABG66144;
 XX DT 29-AUG-2002 (first entry)
 XX DE Ige Fcepsilon RI binding peptide from phage displayed library #1.
 XX KW Ige receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
 KW protein co-ordinate data; Ige-mediated disease; allergic rhinitis;
 KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
 KW parasitic infection; Ige myeloma; immune-related disorder;
 KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
 KW Ige-mediated gastrointestinal inflammatory disease; burn;
 KW immune rejection of graft; myocardial infarction; atherosclerosis;
 KW acute lung injury; haemorrhagic shock; septic shock;
 KW acute tubular necrosis; endometriosis; degenerative joint disease;

KW pancreatitis.
 XX OS Synthetic.
 XX PN WO200226781-A2.
 XX PD 04-APR-2002.
 XX PF 26-SEP-2001; 2001WO-US030289.
 XX PR 26-SEP-2000; 2000US-0235353P.
 XX PR 23-MAR-2001; 2001US-0278540P.
 XX PA (GETH) GENENTECH INC.
 XX PI Lowman HB, Reynolds ME, Nakamura GR, Starovassnik MA;
 XX WI 2002-444016/47.
 XX PT A peptide useful for treating a Ige-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
 PT for binding to high affinity Ige receptor in an in vitro assay.
 XX PS Example 6; Page 97; 328pp; English.
 XX CC The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) E 134 comprising a sequence (SI), for binding the high affinity Ige
 CC receptor (FcepsilonRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface structure
 CC of the peptide, a compound with a solvent accessible surface that mimics
 CC the solvent accessible surface defined by the side chains of residues (R)
 CC Pro4, Phe6, Pro16, Cys3, Cys15 and Cys19 of Ige134, a peptide with
 CC structural coordinates as given in the specification, selecting a peptide
 CC mimetic which binds to FcepsilonRI and blocks binding of Ige and a
 CC peptide mimetic which mimics the coordinates of Ige134 residues (R). (C)
 CC is useful for inhibiting the binding of Ige to high affinity Ige receptor
 CC (FcepsilonRI). Peptides of the formula given in the specification are
 CC useful for inhibiting the binding of an Ige to high affinity Ige
 CC receptor. The peptide is useful for selecting a molecule which blocks the
 CC interaction of Ige with high affinity Ige receptor. The peptide is also
 CC useful for inhibiting the activation of high affinity Ige receptor. The
 CC peptide is useful for treating an Ige-mediated disease or disorder in a
 CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
 CC methods. The peptide is also useful for inhibiting Ige-mediated or
 CC associated processes such as Ige-dependent activation and degranulation
 CC of mast cells and basophils, as well as consequent release of
 CC inflammatory mediators such as histamine. (C) is useful for treating
 CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
 CC urticaria-angioedema, parasitic infection, Ige myeloma, immune-related
 CC disorders, inflammatory disorders, diabetes mellitus, Ige-mediated
 CC gastrointestinal inflammatory disease, immune rejection of grafts,
 CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
 CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
 CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
 CC present sequence is a peptide of the invention expressed from a phage
 CC display library
 XX SQ Sequence 13 AA;
 Query Match 47.4%; Score 27.5; DB 5; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 3 GP-CWVSM 9
 DB 6 GPWGVCM 13
 RESULT 34
 ABG66104
 ID ABG66104 standard; peptide; 13 AA.

XX ABG66104;
XX
XX
DT 29-AUG-2002 (first entry)
XX
DE IGE Fcepsilon RI binding peptide from phage displayed g8 library IGE69.
XX
KW IGE receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
KW protein co-ordinate data; IGE-mediated disease; allergic rhinitis;
KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
KW parasitic infection; IGE myeloma; immune-related disorder;
KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
KW IGE-mediated gastrointestinal inflammatory disease; burn;
KW immune rejection of graft; myocardial infarction; atherosclerosis;
KW acute lung injury; haemorrhagic shock; septic shock;
KW acute tubular necrosis; endometriosis; degenerative joint disease;
KW pancreatitis.
XX
XX Synthetic.
XX
XX WO200226781-A2.
XX
XX PD 04-APR-2002.
XX
XX
XX 26-SEP-2001; 2001WO-US030289.
XX
XX
XX 26-SEP-2000; 2000US-0235353P.
XX
XX 23-MAR-2001; 2001US-0278540P.
XX
XX (GETH) GENENTECH INC.
XX
XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
XX
XX WPI; 2002-444016/47.
XX
XX
XX A peptide useful for treating a IGE-mediated disease or disorder in a
XX host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
XX for binding to high affinity IGE receptor in an in vitro assay.
XX
XX Example 4; Page 87; 328pp; English.
XX
XX The invention relates to a peptide which competes with immunoglobulin
XX (Ig) E 134 comprising a sequence (S1), for binding the high affinity IGE
XX receptor (FcepsilonRI) in an in vitro assay and having a formula given in
XX the specification. Also included are a fusion protein comprising the
XX peptide, a pharmaceutical composition (C) comprising the peptide,
XX designing a compound that mimics the three-dimensional surface structure
XX of the peptide, a compound with a solvent accessible surface that mimics
XX the solvent accessible surface defined by the side chains of residues (R)
XX Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134, a peptide with
XX structural coordinates as given in the specification, selecting a peptide
XX mimetic which binds to FcepsilonRI and blocks binding of IGE and a
XX peptide mimetic which mimics the coordinates of IGE134 residues (R). (C)
XX is useful for inhibiting the binding of IGE to high affinity IGE receptor
XX (FcepsilonRI). Peptides of the formula given in the specification are
XX useful for inhibiting the binding of an IGE to high affinity IGE
XX receptor. The peptide is useful for selecting a molecule which blocks the
XX interaction of IGE with high affinity IGE receptor. The peptide is also
XX useful for inhibiting the activation of high affinity IGE receptor. The
XX peptide is useful for treating an IGE-mediated disease or disorder in a
XX host. (C) is useful in research, diagnostic, therapeutic and prophylactic
XX methods. The peptide is also useful for inhibiting IGE-mediated or
XX associated processes such as IGE-dependent activation and degranulation
XX of mast cells and basophils, as well as consequent release of
XX inflammatory mediators such as histamine. (C) is useful for treating
XX allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
XX urticaria-angioedema, parasitic infection, diabetes mellitus, immune-related
XX disorders, inflammatory disorders, immune rejection of grafts,
XX gastrointestinal inflammatory disease, immune rejection of grafts,
XX reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
XX lung injury, haemorrhagic shock, burn, septic shock, acute tubular
XX necrosis, endometriosis, degenerative joint disease and pancreatitis. The
XX present sequence is a peptide of the invention expressed from a phage

CC display library
XX
XX SQ Sequence 13 AA;
XX
XX Query Match 47.4%; Score 27.5; DB 5; Length 13;
XX Best Local Similarity 75.0%; Pred. No. 6.3e+02;
XX Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX QY 3 GP-GWVSM 9
XX || || || ||
XX Db 6 GPWGWVCM 13
XX
XX
XX RESULT 35
XX ABG66135
XX ID ABG66135 standard; peptide; 14 AA.
XX
XX AC ABG66135;
XX
XX 29-AUG-2002 (first entry)
XX
XX DE IGE Fcepsilon RI binding peptide from phage displayed g8 library IGE107.
XX
XX KW IGE receptor; immunoglobulin; FcepsilonRI; antagonist; phage display;
XX protein co-ordinate data; IGE-mediated disease; allergic rhinitis;
XX asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;
XX parasitic infection; IGE myeloma; immune-related disorder;
XX inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
XX IGE-mediated gastrointestinal inflammatory disease; burn;
XX immune rejection of graft; myocardial infarction; atherosclerosis;
XX acute lung injury; haemorrhagic shock; septic shock;
XX acute tubular necrosis; endometriosis; degenerative joint disease;
XX pancreatitis.
XX
XX OS Synthetic.
XX
XX XX WO200226781-A2.
XX
XX XX PD 04-APR-2002.
XX
XX XX 26-SEP-2001; 2001WO-US030289.
XX
XX XX 26-SEP-2000; 2000US-0235353P.
XX
XX XX 23-MAR-2001; 2001US-0278540P.
XX
XX XX (GETH) GENENTECH INC.
XX
XX XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
XX
XX XX WPI; 2002-444016/47.
XX
XX XX
XX XX A peptide useful for treating a IGE-mediated disease or disorder in a
XX host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
XX for binding to high affinity IGE receptor in an in vitro assay.
XX
XX XX Example 4; Page 88; 328pp; English.
XX
XX XX The invention relates to a peptide which competes with immunoglobulin
XX (Ig) E 134 comprising a sequence (S1), for binding the high affinity IGE
XX receptor (FcepsilonRI) in an in vitro assay and having a formula given in
XX the specification. Also included are a fusion protein comprising the
XX peptide, a pharmaceutical composition (C) comprising the peptide,
XX designing a compound that mimics the three-dimensional surface structure
XX of the peptide, a compound with a solvent accessible surface that mimics
XX the solvent accessible surface defined by the side chains of residues (R)
XX Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGE134, a peptide with
XX structural coordinates as given in the specification, selecting a peptide
XX mimetic which binds to FcepsilonRI and blocks binding of IGE and a
XX peptide mimetic which mimics the coordinates of IGE134 residues (R). (C)
XX is useful for inhibiting the binding of IGE to high affinity IGE receptor
XX (FcepsilonRI). Peptides of the formula given in the specification are
XX useful for inhibiting the binding of an IGE to high affinity IGE
XX receptor. The peptide is useful for selecting a molecule which blocks the

XX
DE 26-SEP-2001. 2001W0-115030289

XX 26-SEP-2000; 2000US-0235353P.
 PR 23-MAR-2001; 2001US-0278540P.
 XX (GETH) GENENTECH INC.
 XX Lowman HB, Reynolds ME, Nakamura GR, Starovasnik MA;
 PI WPI; 2002-444016/47.
 XX
 XX A peptide useful for treating a IgE-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin E
 PT for binding to high affinity IgE receptor in an in vitro assay.
 XX
 XX Example 4; Page 87; 328pp; English.
 XX
 XX The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) E 134 comprising a sequence (S1), for binding the high affinity IgE
 CC receptor (FcεRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface structure
 CC of the peptide, a compound with a solvent accessible surface that mimics
 CC the solvent accessible surface defined by the side chains of residues (R)
 CC Pro4, Phe6, Prol6, Cys7, Cys15 and Cys19 of IgE134, a peptide with
 CC structural coordinates as given in the specification, selecting a peptide
 CC mimetic which binds to FcεRI and blocks binding of IgE and a
 CC peptide mimetic which mimics the coordinates of IgE and a
 CC (FcεRI) receptor. Peptides of the formula given in the specification are
 CC useful for inhibiting the binding of an IgE to high affinity IgE
 CC receptor. The peptide is useful for selecting a molecule which blocks the
 CC interaction of IgE with high affinity IgE receptor. The peptide is also
 CC useful for inhibiting the activation of high affinity IgE receptor. The
 CC peptide is useful for treating an IgE-mediated disease or disorder in a
 CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
 CC methods. The peptide is also useful for inhibiting IgE-mediated or
 CC associated processes such as IgE-dependent activation and degranulation
 CC of mast cells and basophils, as well as consequent release of
 CC inflammatory mediators such as histamine. (C) is useful for treating
 CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
 CC urticaria-angioedema, parasitic infection, IgE myeloma, immune-related
 CC disorders, inflammatory disorders, diabetes mellitus, IgE-mediated
 CC gastrointestinal inflammatory disease, immune rejection of grafts,
 CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
 CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
 CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
 CC present sequence is a peptide of the invention expressed from a phage
 CC display library
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 47.4%; Score 27.5; DB 5; Length 14;
 Best Local Similarity 75.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 3 GP-GWVSM 9
 DB 7 GPWGVCVM 14
 |||||
 |||||
 RESULT 38
 AAEE34589
 ID AAEE34589 standard; peptide; 8 AA.
 XX
 XX AAEE34589;
 AC
 XX
 XX 14-MAY-2003 (first entry)
 DT
 XX
 DE Phage peptide #4 from CL6 library.
 XX
 XX CERVIG protein; signal regulatory protein; autoimmune syndrome;
 KW SIRPalpa; inflammation; urinary disease; central nervous system disease;

KW immune disease; Gastrointestinal tract disease; TH1-type immune response;
 KW graft versus host disease; pulmonary disease; REC destruction; memory;
 KW autoimmune haemolytic anaemia; gene therapy; nephrotropic; neurotropic;
 XX immunosuppressive.
 OS Unidentified.
 XX WO200292784-A2.
 PN
 XX 21-NOV-2002.
 PD
 XX 15-MAY-2002; 2002WO-US018531.
 PF
 XX 15-MAY-2001; 2001US-0291050P.
 PR
 XX (UYEM-) UNIV EMORY.
 PA
 XX Parkos CA;
 PI
 XX WPI; 2003-120676/11.
 DR
 XX New isolated CERVIG polypeptide, useful for modulating SIRPalpa-CD47
 PT functions and in treating conditions such as inflammation, graft versus
 PT host disease and autoimmune syndromes.
 XX
 XX Example 1; Page 45; 104pp; English.
 XX
 XX The invention relates to CERVIG proteins and polynucleotides encoding
 CC such proteins. Sequences of the invention are useful in modulating signal
 CC regulatory proteins (SIRP) alpha-CD47 functions and in treating conditions
 CC such as inflammation, pulmonary diseases, urinary diseases, central
 CC nervous system diseases, immune diseases and gastrointestinal tract
 CC diseases. They are particularly used to inhibit the development of TH1-
 CC type immune response, undesirable effects of graft versus host disease
 CC and autoimmune syndromes, inhibit inappropriate RBC destruction in
 CC autoimmune haemolytic anaemia or related diseases and improve memory.
 CC CERVIG sequences are also used in gene therapy. The present sequence is a
 CC phage peptide used in the exemplification of the invention
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 46.6%; Score 27; DB 6; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HVGPCW 6
 DB 2 HPGTGW 7
 |||||
 |||||
 RESULT 39
 AAB70713
 ID AAB70713 standard; peptide; 9 AA.
 XX
 XX AAB70713;
 AC
 XX 14-MAY-2001 (first entry)
 DT
 XX
 DE Human TAA R11 immunogenic peptide fragment SEQ ID 38.
 XX
 XX TAA; tumor associated antigen; R11; immunogenic; anticancer; vaccine;
 KW cellular immune response; humoral immune response; cancer cell;
 KW immunotherapy; cancer; cytostatic agent; breast carcinoma; diagnosis;
 KW adrenal carcinoma; pancreatic carcinoma.
 XX
 XX Homo sapiens.
 OS
 XX DE19936563-A1.
 PN
 XX 08-FEB-2001.
 PD
 XX 04-AUG-1999; 99DE-01036563.
 PF
 XX

PR 04-AUG-1999; 99DE-01036563.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA Konopitzky R, Koenig U, Sommergruber W, Woelfel T;
 PI WPI; 2001-203694/21.
 XX New tumor-associated antigen R11, useful for immunotherapy of tumors and
 XX for diagnosis, e.g. to assess the immune response to vaccination or for
 XX prognosis of tumors.
 XX Claim 5; Page 32; 46pp; German.
 XX This invention describes a novel tumor-associated antigen designated R11
 XX comprising a 356 amino acid (aa) sequence, as defined in the
 XX specification. The invention also describes (a) immunogenic protein
 XX fragments or peptides (I) derived from R11; (b) isolated DNA (II)
 XX encoding a protein (III) with the immunogenic properties of R11, and its
 XX fragments; (c) recombinant DNA that includes (II); and (d) antibodies
 XX (Ab) directed against R11 or (I). The products of the invention have
 XX anticancer activity and induce specific cellular or humoral immune
 XX response against cancer cells. R11, or derived immunogenic peptides and
 XX (recombinant) nucleic acid encoding them, are used for in vitro or in
 XX vivo immunotherapy of cancers. Cells that express R11 are useful in
 XX cancer vaccines and antibodies (Ab) that recognize R11 are used for
 XX treatment (e.g. when coupled to a cytostatic agent or radioisotope),
 XX diagnosis or monitoring of cancers associated with expression of R11
 XX (particularly breast, adrenal or pancreatic carcinoma). R11-derived
 XX peptides can also be used for diagnosis, e.g. to assess the immune
 XX response to vaccination or for prognosis of tumors
 XX
 XX Sequence 9 AA;
 QY Query Match 46.6%; Score 27; DB 4; Length 9;
 DB Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GPGWVS 8
 DB 3 GPRWLS 8
 RESULT 40
 AAR31271
 ID AAR31271 standard; peptide; 10 AA.
 AC AAR31271;
 XX 12-FEB-1993 (first entry)
 XX HIV principal determinant peptide.
 XX AIDS; ARC; human immunodeficiency virus; vaccine; cyclic; Neisseria;
 KW meningitidis b; outer membrane protein complex; OMPC; cPND30.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /label= Nle
 FT /note= "this position is linked to the OMPC of the
 FT conjugate"
 FT Modified-site 2
 FT /note= "epsilon-amino group is condensed with C-terminal
 FT COOH to form cyclic peptide"
 FT Modified-site 10
 FT /note= "forms amide bond with epsilon-amino of Lys(2) to
 FT give cyclic molecule"
 XX EP467700-A.
 XX 22-JAN-1992.
 PD

XX 19-JUL-1991; 91EP-00306598.
 XX 19-JUL-1990; 90US-00555339.
 PR 19-JUL-1990; 90US-00555966.
 PR 19-JUN-1991; 91US-00715276.
 PR 19-JUN-1991; 91US-00715278.
 XX (MERI) MERCK & CO INC.
 PA Leanza WJ, Marburg S, Tolman RL, Emini EA;
 PI WPI; 1992-026505/04.
 XX Conjugate proteins comprising HIV peptide components - useful for
 XX preparing vaccines for e.g. AIDS or for treating infections.
 XX Claim 12; Page 55; 63pp; English.
 XX The invention relates to a co-conjugate comprising an immunogenic protein
 XX or protein complex having a first set of covalent linkages to low
 XX molecular weight moieties which have an anionic or polyanionic character
 XX at physiological pH, and a second set of covalent linkages to peptides
 XX comprising HIV principal neutralizing determinants (PND's) or
 XX immunologically equivalent peptides. Preferably at least one set of the
 XX covalent linkages is comprised of maleimide derivatives; the
 XX (poly)anionic moiety is composed of one to five residues of the anionic
 XX form of a carboxylic, sulphonic or phosphonic acid; the immunogenic
 XX protein is the outer membrane protein complex (OMPC) of Neisseria
 XX meningitidis b; and the PND peptide has a linear structure, a disulphide-
 XX bonded cyclic structure, an amide-bonded cyclic structure or a thioether-
 XX bonded cyclic structure. The present sequence (cPND30) is an example of a
 XX PND peptide component used in the co-conjugate. The co-conjugate is
 XX useful for inducing anti-peptide immune response in mammals, for inducing
 XX HIV-neutralizing antibodies in mammals, for formulating vaccines to
 XX prevent HIV infection or disease, including AIDS, or for treating humans
 XX afflicted with HIV infection or disease
 XX
 XX Sequence 10 AA;
 QY Query Match 46.6%; Score 27; DB 2; Length 10;
 DB Best Local Similarity 71.4%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPCWV 7
 DB 3 HIGFGRV 9
 RESULT 41
 AAR31308
 ID AAR31308 standard; peptide; 10 AA.
 AC AAR31308;
 XX 11-FEB-1993 (first entry)
 XX Cyclic HIV principal neutralizing determinant peptide.
 XX Human immunodeficiency virus; PND; cyclic; conjugate; AIDS; vaccine;
 KW immunogen; ELISA; analysis; cPND30.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /label= Nle
 FT /note= "Z-Nle"
 FT Modified-site 2 /note= "forms cyclic lactam bond, via epsilon-NH2, with C
 FT -terminal COOH"
 FT Modified-site 10 /note= "forms cyclic amide bond with epsilon- NH2 of
 FT

FT XX Lys (2)"

FN EP471453-A.

PD 19-FEB-1992.

XX 19-JUL-1991; 91EP-00306582.

XX 19-JUL-1990; 90US-00555112.

PR 19-JUL-1990; 90US-00555112.

XX (MERI) MERCK & CO INC.

XX Sugg EE, Dolan CA, Bednarek MA, Tolman RL, Christensen BG;

PI WPI; 1992-058511/08.

XX New cyclic HIV principal neutralising determinant peptide(s) - used as

XX laboratory tools and as vaccines against HIV, AIDS, arc etc.

XX Claim 4; Page 22; 25pp; English.

XX The peptide (cPND30) is a specifically claimed example of HIV principal

CC neutralizing determinant peptides which are covered generically in Claims

CC 1-3 (AAR31291, AAR31292), the peptides being stably cyclised as a result

CC of a lactam bridge between an NH2 on the N-terminal side of the loop

CC amino acids and a COOH on the C-terminal side of the loop amino acids.

CC The bond is less labile than a disulphide bond. The stable cyclic HIV PND

CC peptides (cPND's) may be used as analytical tools and as reagents in

CC ELISA assays. They may also be conjugated to an immunogenic carrier (a

CC protein and/or a polysaccharide; e.g. PRP or OMP) to give a product

CC useful for inducing mammalian anti-peptide, anti-HIV, or HIV-neutralizing

CC immune responses and for formulating vaccines to prevent HIV disease,

CC including AIDS and ARC, or for treating humans afflicted with HIV disease

CC such as AIDS or ARC

XX Sequence 10 AA;

Query Match 46.6%; Score 27; DB 2; Length 10;

Best Local Similarity 71.4%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7

Db 3 HIGPGRV 9

RESULT 42

AAR26707

ID AAR26707 standard; peptide; 10 AA.

XX AAR26707;

XX 09-FEB-1993 (first entry)

XX HIV-PND-polysaccharide-protein conjugate vaccine.

XX Human immunodeficiency virus; principal neutralizing determinant;

XX outer membrane protein complex; OMP; Neisseria; AIDS; cyclic; cPND30.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /label= Nle

FT /note= "bonded via N-terminal to polysaccharide- protein

FT complex"

FT Modified-site 2

FT /note= "epsilon-amino forms cyclic peptide with C-

FT terminal COOH group"

FT Modified-site 10

FT /note= "condenses with side chain NH2 of Lys(2) to give

FT cyclic peptide"

XX

PN EP468714-A.

XX 29-JAN-1992.

XX 19-JUL-1990; 90US-00555558.

XX 19-JUL-1990; 90US-00555558.

PR 19-JUL-1990; 90US-00555974.

PR 19-JUN-1991; 91US-00715275.

PR 19-JUN-1991; 91US-00715277.

XX (MERI) MERCK & CO INC.

XX Marburg S, Tolman RL, Emini EA;

XX WPI; 1992-034437/05.

XX HIV peptide-polysaccharide-protein conjugates - used in vaccines or to

XX produce antibodies to prevent or treat HIV infection.

XX Claim 9; Page 56; 63pp; English.

XX The invention relates to a conjugate of an HIV principal neutralizing

CC determinant (PND), or an immunologically equivalent peptide (PEP),

CC covalently coupled to an immunogenic protein or protein complex through

CC an anionic polysaccharide linker. Pref. the immunogenic protein is the

CC outer membrane protein complex (OMPC) of Neisseria meningitidis b and the

CC PND peptide has a linear structure, a disulphide-bonded cyclic structure,

CC an amide-bonded cyclic structure or a thioether-bonded cyclic structure.

CC The present sequence (cPND30) is an example of a PND peptide component.

CC The conjugates are used for inducing HIV-neutralising antibodies or for

CC making vaccines to prevent contraction of HIV infection or disease. The

CC antibodies can be used for passively protecting against infection by HIV,

CC or for protecting against proliferation of HIV post-infection, or for

CC treating AIDS, or in diagnostic assays

XX Sequence 10 AA;

Query Match 46.6%; Score 27; DB 2; Length 10;

Best Local Similarity 71.4%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYGPGWV 7

Db 3 HIGPGRV 9

RESULT 43

AAW08545

ID AAW08545 standard; protein; 11 AA.

XX AAW08545;

XX 23-SEP-1997 (first entry)

XX C6 human sFv antibody C6.5 variable light chain CDR3 mutant C6ML3-17.

XX Tumour; immune response; cytotoxin; carcinoma; breast cancer.

XX Homo sapiens.

XX Synthetic.

XX WO9700271-A1.

XX 03-JAN-1997.

XX 13-JUN-1996; 96WO-US010287.

XX 14-JUN-1995; 95US-0000238P.

PR 15-JUN-1995; 95US-0000250P.

XX (REGC) UNIV CALIFORNIA.

XX

PI Marks JD, Schier R;
 XX WPI; 1997-077488/07.
 DR
 XX
 PT New C6 human antibody binding specifically to c-erbB-2 - useful for
 PT treatment and diagnosis of tumours, with reduced risk of generating
 PT immune response.
 XX
 XX
 PS Claim 10; Page 93; 117pp; English.
 XX
 XX The present sequence represents a variable light chain CDR3 mutant C6ML3-
 CC 17 modified from the derived light chain variable region of the C6 human
 CC antibody C6.5. The mutant C6ML3-17 specifically binds to c-erbB-2. A
 CC chimeric molecule that binds specifically to tumour cells carrying c-erbB
 CC -2 consists of an effector compound attached to a C6 human antibody. If
 CC the effector compound is a cytotoxin the chimeric molecule can be used to
 CC inhibit growth of c-erbB-2 positive tumours (especially breast and other
 CC carcinomas). If the effector compound is a label the chimeric molecule
 CC can be used to detect such cells, including in vivo localisation. The
 CC antibody can also be used for diagnosis/localisation, in vivo or in
 CC vitro, especially by immunoassay. The nucleic acid encoding the antibody,
 CC and a nucleic acid encoding a single chain polypeptide with the binding
 CC specificity of the antibody and comprising the binding portions of
 CC variable regions of light and heavy chains of the antibody, joined by a
 CC linker, can be used to produce recombinant proteins by standard methods.
 CC Unlike known anti-c-erbB-2 antibodies, C6 antibodies are fully human, so
 CC should elicit little, if any, immunogenic response
 XX
 SQ Sequence 11 AA;
 Query Match 46.6%; Score 27; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPQWV 7
 Db :| |||
 5 YYRSGWV 11
 RESULT 44
 AAW08535
 ID AAW08535 standard; protein; 11 AA.
 AC AAW08535;
 XX
 DT 23-SEP-1997 (first entry)
 XX
 XX C6 human sFv antibody C6.5 variable light chain CDR3 mutant C6ML3-16.
 XX Tumour; immune response; cytotoxin; carcinoma; breast cancer.
 KW Homo sapiens.
 OS Synthetic.
 OS WO9700271-A1.
 EN
 XX
 XX 03-JAN-1997.
 XX
 XX 13-JUN-1996; 96WO-US010287.
 XX
 XX 14-JUN-1995; 95US-0000238P.
 PR 15-JUN-1995; 95US-0000250P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Marks JD, Schier R;
 PI WPI; 1997-077488/07.
 DR
 XX New C6 human antibody binding specifically to c-erbB-2 - useful for
 PT treatment and diagnosis of tumours, with reduced risk of generating
 PT immune response.
 PT
 XX

PS Claim 10; Page 93; 117pp; English.
 XX
 XX The present sequence represents a variable light chain CDR3 mutant C6ML3-
 CC 16 modified from the derived light chain variable region of the C6 human
 CC antibody C6.5. The mutant C6ML3-16 specifically binds to c-erbB-2. A
 CC chimeric molecule that binds specifically to tumour cells carrying c-erbB
 CC -2 consists of an effector compound attached to a C6 human antibody. If
 CC the effector compound is a cytotoxin the chimeric molecule can be used to
 CC inhibit growth of c-erbB-2 positive tumours (especially breast and other
 CC carcinomas). If the effector compound is a label the chimeric molecule
 CC can be used to detect such cells, including in vivo localisation. The
 CC antibody can also be used for diagnosis/localisation, in vivo or in
 CC vitro, especially by immunoassay. The nucleic acid encoding the antibody,
 CC and a nucleic acid encoding a single chain polypeptide with the binding
 CC specificity of the antibody and comprising the binding portions of
 CC variable regions of light and heavy chains of the antibody, joined by a
 CC linker, can be used to produce recombinant proteins by standard methods.
 CC Unlike known anti-c-erbB-2 antibodies, C6 antibodies are fully human, so
 CC should elicit little, if any, immunogenic response
 XX
 SQ Sequence 11 AA;
 Query Match 46.6%; Score 27; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HYGPQWV 7
 Db :| |||
 5 YYRSGWV 11
 RESULT 45
 ADC44682
 ID ADC44682 standard; peptide; 12 AA.
 XX
 AC ADC44682;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 XX Endothelial cell binding peptide SEQ ID NO:411.
 DE endothelial cell binding protein; ECEP; anti-tumour; cytostatic;
 KW vasotropic; antipsoriatic; dermatological; ophthalmological;
 KW antidiabetic; antiarthritic; vulnary; antitumor; antiinflammatory;
 KW antibacterial; gynaecological; angiogenesis.
 XX
 OS Synthetic.
 OS WO2003037172-A2.
 PN
 XX 08-MAY-2003.
 PD
 XX 01-NOV-2002; 2002WO-US035258.
 PF
 XX 01-NOV-2001; 2001US-0334822P.
 PR
 XX (GPCB-) GPC BIOTECH INC.
 PA
 XX Gyuris J, Lamphere L, Morris AJ, Tsaion K;
 PI WPI; 2003-482072/45.
 XX
 XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
 PT proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 XX
 PS Claim 3; SEQ ID NO 411; 126pp; English.
 XX
 XX The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECEP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasotropic, antipsoriatic, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnary, antitumor,
 CC

CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an ECBP agonist which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an ECBP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by administering an ECBP agonist or
 CC ECBP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECBP sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECBP of the
 CC invention.

XX
 SQ Sequence 12 AA;

Query Match 46.6%; Score 27; DB 7; Length 12;
 Best Local Similarity 50.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 HYGPGWVS 8
 | | | |
 Db 3 HQASGWTS 10

Search completed: August 30, 2004, 10:49:37
 Job time : 15.4088 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 14.8986 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-9

Perfect score: 55

Sequence: 1 FFITTVKTAW 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	3	AAy69929 Human cyc
2	49	89.1	10	3	AAy69949 Human cyc
3	30	54.5	8	3	AAy69948 Human cyc
4	30	54.5	13	6	ABU11914 Human HGP
5	30	54.5	13	6	ABU11931 Human HGP
6	29	52.7	14	4	AAg98085 Human SNP
7	29	52.7	14	4	AAb29764 Equus sp.
8	27	49.1	13	2	AAw78212 Human sec
9	25.5	46.4	11	4	ABP18094 HIV B58 s
10	25	45.5	9	4	ABP21178 HIV A03 m
11	25	45.5	9	4	ABP13475 HIV A02 s
12	25	45.5	9	5	AAU94469 Human nov
13	25	45.5	9	5	AAU94677 Human nov
14	25	45.5	9	5	AAU94889 Human nov
15	25	45.5	10	4	ABP21186 HIV A03 m
16	25	45.5	10	4	ABP11874 HIV A01 s
17	25	45.5	10	4	ABP16363 HIV A24 s
18	25	45.5	10	5	ABP61558 Human KRP
19	25	45.5	10	5	AAm47755 p36 trypt
20	25	45.5	10	5	ABg98537 F protein
21	25	45.5	10	5	ABg98536 F protein
22	25	45.5	10	5	AAU95405 Human nov
23	25	45.5	10	5	AAU94768 Human nov
24	25	45.5	10	5	AAU94575 Human nov
25	25	45.5	10	5	AAU95402 Human nov

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26 25 45 5 12 7 ADC44696
27 25 45 5 13 3 AAB38906
28 25 45 5 13 3 AAB38906
29 24 43 6 10 2 AAR79122
30 24 43 6 10 2 AAW09941
31 24 43 6 10 4 AAG86162
32 24 43 6 11 2 AAW21219
33 24 43 6 11 4 AAM97289
34 24 43 6 12 2 AAR52697
35 24 43 6 12 2 AAR52696
36 24 43 6 12 6 ABP99066
37 24 43 6 12 6 ABU14354
38 24 43 6 12 6 ABU14171
39 24 43 6 12 6 ABU14170
40 24 43 6 12 6 ABU14355
41 24 43 6 12 6 ABU14172
42 24 43 6 12 6 ABU14353
43 24 43 6 12 6 ABU14173
44 24 43 6 13 3 AAB38907
45 24 43 6 13 3 AAB38843

```

ALIGNMENTS

RESULT 1

AAy69929
ID AAY69929 standard; peptide; 10 AA.

XX AC AAY69929;

XX AC AC

DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #9.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX FN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH)/ ITOH K.

XX PI Itoh K, Gomi S;

XX DR WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and

XX PT diagnosis of tumors.

XX PS Claim 4; Page 51; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The

XX CC peptides are tumour antigen peptides derived from cyclophilin B, that

XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The

XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 10 AA;

XX SQ Query Match 100.0%; Score 55; DB 3; Length 10;

XX SQ Best Local Similarity 100.0%; Pred. No; 0.0026;

XX SQ Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 FFITTVKTAW 10

Db 1 FFTVKTAW 10

RESULT 2

AA69949
ID AAY69949 standard; peptide; 10 AA.

AC AAY69949;

XX 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #29.

DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO9967288-A1.

XX 29-DEC-1999.

PF 24-JUN-1999; 99WO-JP003360.

PR 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumors.

XX Claim 4; Page 57; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 10 AA;

Query Match 89.1%; Score 49; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.031; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 2 FFTVKTAW 10

|||||

Db 1 FFTVKTAW 9

RESULT 3

AA69948

ID AAY69948 standard; peptide; 8 AA.

XX AC AAY69948;

XX 11-APR-2000 (first entry)

XX Human cyclophilin B peptide fragment #28.

DE Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO9967288-A1.

XX 29-DEC-1999.

XX

PF 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

PA (ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and

PT diagnosis of tumors.

XX Claim 4; Page 56; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 8 AA;

Query Match 54.5%; Score 30; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+06; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0;

QY 1 FFTTV 6

|||||

Db 3 FFTTV 8

RESULT 4

ABU11914

ID ABU11914 standard; peptide; 13 AA.

XX AC ABU11914;

XX 13-FEB-2003 (first entry)

XX Human HGPRMY11 PKC phosphorylation site #1.

XX Human; immunogen; HGPRMY11; HGPRMY11v1; HGPRMY11v2; GPCR74; GPCR81;

KW G-protein coupled receptor; cardiovascular disease; arrhythmia;

KW myocardial infarction; congestive heart failure; cardiomyopathy;

KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;

KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;

KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;

KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;

KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.

XX Homo sapiens.

XX WO200286123-A2.

XX 31-OCT-2002.

XX 16-NOV-2001; 2001WO-US044019.

XX 17-NOV-2000; 2000US-0249613P.

XX 21-DEC-2000; 2000US-0257611P.

XX 16-JUL-2001; 2001US-0305818P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;

XX WPI; 2003-093137/08.

XX New human G-protein coupled receptor HGPRMY11 polypeptide or

PT polynucleotide, useful for preventing, treating or ameliorating e.g.

PT myocardial infarction, angina, thrombosis, Alzheimer's disease,

PT schizophrenia, AIDS, leukemia.

XX PS Disclosure; Page 48; 444pp; English.

XX XX The invention relates to an isolated polypeptide (designated HGPRBMV11),

CC CC which has a G-protein coupled receptor (GPCR) activity (also known as

CC CC GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit

CC CC Number PTA-2766, its variants (HGPRBMV11v1 and HGPRBMV11v2), fragments,

CC CC domains, species homologues and proteins 95% similar to it. Also included

CC CC are: (1) the nucleic acids encoding the HGPRBMV11 proteins (including

CC CC variants, fragments, complements and sequences 95% similar to the

CC CC HGPRBMV11 nucleic acids); (2) recombinant vectors; (3) transformed host

CC CC cells expressing HGPRBMV11; (4) an anti-HGPRBMV11 antibody; (5)

CC CC diagnosing a pathological condition or a susceptibility to a pathological

CC CC condition in a subject; (6) identifying a binding partner to the

CC CC HGPRBMV11 polypeptide; (7) identifying an activity in a biological assay;

CC CC (8) a process for making polynucleotide sequences encoding a gene product

CC CC having altered GPCR activity; (9) a shuffled polynucleotide produced by

CC CC the method of (8); and (10) screening for candidate compounds capable of

CC CC binding to and/or modulating activity of a GPCR. The polypeptide or the

CC CC polynucleotide is useful for preventing, treating or ameliorating a

CC CC medical condition, particularly cardiovascular diseases or disorders,

CC CC e.g. myocardial infarction, congestive heart failure, arrhythmias,

CC CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,

CC CC thrombosis or hypertension). The HGPRBMV11 polypeptide or polynucleotide

CC CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's

CC CC disease, Parkinson's disease, osteoporosis, obesity, human

CC CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,

CC CC acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,

CC CC inflammations, psoriasis, Gaucher's disease or ischaemia (many other

CC CC diseases and disorders are listed in the specification). The present

CC CC sequence represents a protein motif or domain of an HGPRBMV11 protein (or

CC CC variant) which may be used as an immunogen

XX SQ Sequence 13 AA;

Query Match 54.5%; Score 30; DB 6; Length 13;

Best Local Similarity 37.5%; Pred. No. 1e+02;

Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10

Db 4 VTSIRSAW 11

RESULT 5

ABU11931

ID ABU11931 standard; peptide; 13 AA.

AC ABU11931;

XX 13-FEB-2003 (first entry)

DE Human HGPRBMV11v1 PKC phosphorylation site #1.

XX Human; immunogen; HGPRBMV11; HGPRBMV11v1; HGPRBMV11v2; GPCR74; GPCR81;

KW G-protein coupled receptor; cardiovascular disease; arrhythmia;

KW myocardial infarction; congestive heart failure; cardiomyopathy;

KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;

KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;

KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;

KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;

KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.

OS Homo sapiens.

XX WO200286123-A2.

PN 31-OCT-2002.

XX 16-NOV-2001; 2001WO-US044019.

XX 17-NOV-2000; 2000US-0249613P.

PR 21-DEC-2000; 2000US-0257611P.

PR 16-JUL-2001; 2001US-0305818P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;

XX WPI; 2003-093137/08.

XX New human G-protein coupled receptor HGPRBMV11 polypeptide or

PT polynucleotide, useful for preventing, treating or ameliorating e.g.

PT myocardial infarction, angina, thrombosis, Alzheimer's disease,

PT schizophrenia, AIDS, leukemia.

XX Disclosure; Page 76; 444pp; English.

XX The invention relates to an isolated polypeptide (designated HGPRBMV11),

CC CC which has a G-protein coupled receptor (GPCR) activity (also known as

CC CC GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit

CC CC Number PTA-2766, its variants (HGPRBMV11v1 and HGPRBMV11v2), fragments,

CC CC domains, species homologues and proteins 95% similar to it. Also included

CC CC are: (1) the nucleic acids encoding the HGPRBMV11 proteins (including

CC CC variants, fragments, complements and sequences 95% similar to the

CC CC HGPRBMV11 nucleic acids); (2) recombinant vectors; (3) transformed host

CC CC cells expressing HGPRBMV11; (4) an anti-HGPRBMV11 antibody; (5)

CC CC diagnosing a pathological condition or a susceptibility to a pathological

CC CC condition in a subject; (6) identifying a binding partner to the

CC CC HGPRBMV11 polypeptide; (7) identifying an activity in a biological assay;

CC CC (8) a process for making polynucleotide sequences encoding a gene product

CC CC having altered GPCR activity; (9) a shuffled polynucleotide produced by

CC CC the method of (8); and (10) screening for candidate compounds capable of

CC CC binding to and/or modulating activity of a GPCR. The polypeptide or the

CC CC polynucleotide is useful for preventing, treating or ameliorating a

CC CC medical condition, particularly cardiovascular diseases or disorders,

CC CC e.g. myocardial infarction, congestive heart failure, arrhythmias,

CC CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,

CC CC thrombosis or hypertension). The HGPRBMV11 polypeptide or polynucleotide

CC CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's

CC CC disease, Parkinson's disease, osteoporosis, obesity, human

CC CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,

CC CC acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,

CC CC inflammations, psoriasis, Gaucher's disease or ischaemia (many other

CC CC diseases and disorders are listed in the specification). The present

CC CC sequence represents a protein motif or domain of an HGPRBMV11 protein (or

CC CC variant) which may be used as an immunogen

XX SQ Sequence 13 AA;

Query Match 54.5%; Score 30; DB 6; Length 13;

Best Local Similarity 37.5%; Pred. No. 1e+02;

Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10

Db 4 VTSIRSAW 11

RESULT 6

AAG98085

ID AAG98085 standard; peptide; 14 AA.

XX AAG98085;

XX 19-SEP-2001 (first entry)

DE Human SNP associated peptide SEQ ID NO. 727.

XX Human; single nucleotide polymorphism; SNP; angiotensin;

KW 4-hydroxybutyrate; dehydrogenase; protein therapy;

KW adenosine triphosphate-dependent RNA helicase;

KW major histocompatibility complex Class I histocompatibility antigen; MHC;

KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;

KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;

KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.

XX OS Homo sapiens.
 XX PN WO200148245-A2.
 XX PD 05-JUL-2001.
 XX PF 27-DEC-2000; 2000WO-US035346.
 XX PR 27-DEC-1999; 99US-00472688.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shimkets RA, Leach M;
 XX DR WPI; 2001-418297/44.
 XX PT Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
 PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
 PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
 PT diseases and infections.
 XX PS Disclosure; Page 450; 484pp; English.
 XX CC The invention relates to nucleic acids (AAH79386-AAH80036) encoding
 CC polymorphic variants of proteins (AAG98010-AAG98238) related to
 CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
 CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
 CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
 CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
 CC proteins have potential immunosuppressive, immunostimulatory,
 CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
 CC antileukemic, neuroprotective and antimicrobial activity and may be
 CC useful in gene/protein therapy, vaccines, modulation of the expression
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
 CC histocompatibility complex (MHC) Class I histocompatibility antigen
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include multifactorial
 CC diseases with a genetic component, such as autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of
 CC the bladder, brain, breast, colon and kidney, leukemia), diseases of the
 CC nervous system, an infection of pathogenic organisms. They may also be
 CC used to alter phenotypic traits such as longevity, appearance, strength,
 CC speed and endurance
 XX SQ Sequence 14 AA;
 Query Match 52.7%; Score 29; DB 4; Length 14;
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TTVKTAW 10
 |::|::|
 Db 6 TSLATSW 12
 RESULT 7
 AAB29764
 ID AAB29764 standard; peptide; 14 AA.
 AC AAB29764;
 XX 06-AUG-2003 (revised)
 XX 28-FEB-2001 (first entry)
 DT
 DE Equus sp./gundi alpha globin.
 XX Haemoglobin; rHb1.1; bacterial expression;
 KW N-terminal methionine methylation signal; demethylation;
 KW Escherichia coli; non-immunogenic; pharmaceutical composition; horse;
 KW donkey; zebra; kulan; onager; gundi.

XX OS Equus caballus.
 OS Equus asinus.
 OS Equus zebra.
 OS Equus hemionus.
 OS Ctenodactylus gundi.
 XX PN US6140071-A.
 XX PD 31-OCT-2000.
 XX PF 27-JAN-1994; 94US-00188374.
 XX PR 27-JAN-1994; 94US-00188374.
 XX PA (SOMA-) SOMATOGEN INC.
 XX PI Aitken JF, Apostol IZ, Levine JD, Lippincott JA;
 XX DR WPI; 2001-048257/06.
 XX PT Decreasing methylation of an N-terminus protein, especially hemoglobin
 PT having proline at amino acid position 4, useful for producing
 PT demethylated proteins for treating diseases, by altering this amino acid
 PT to a non-proline residue.
 XX PS Disclosure; Col 5; 26pp; English.
 XX CC The invention relates to a method of decreasing the amount of N-terminal
 CC methionine methylation on a protein expressed in a bacterium. The
 CC bacterial methyltransferase which directs N-terminal methionine
 CC methylation recognises proteins which have a proline residue at position
 CC 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis
 CC protein CheZ). The method comprises introducing mutations into the DNA
 CC encoding the protein so that residue 4 is a non-proline residue, thereby
 CC reducing the degree of N-terminal methylation when the protein is
 CC expressed in a bacterium. The method is useful for decreasing methylation
 CC of a protein, particularly a recombinantly produced protein. The
 CC demethylated protein can be used in a pharmaceutical composition for the
 CC treatment of a disease but with less likelihood of eliciting an
 CC immunological response. These demethylated proteins may be used as
 CC therapeutic agent for the treatment and/or amelioration of disease or
 CC symptoms associated with a disease. The exemplifications describe the
 CC expression of a recombinant human haemoglobin construct (rHb1.1) in
 CC Escherichia coli and its modification such that residue 4 of the di-
 CC alpha chain of the recombinant haemoglobin is altered from proline to a
 CC non-proline residue. The present sequence represents a peptide referred
 CC to in the disclosure of the invention. (Updated on 06-AUG-2003 to correct
 CC OS field.)
 XX SQ Sequence 14 AA;
 Query Match 52.7%; Score 29; DB 4; Length 14;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 TTVKTAW 10
 |::|::|
 Db 8 TNVKAAR 14
 RESULT 8
 AAW78212
 ID AAW78212 standard; protein; 13 AA.
 AC AAW78212;
 XX 13-APR-1999 (first entry)
 DT
 DE Human secreted protein encoded by gene 9 clone HPFCY51.
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW developmental abnormality; foetal deficiency; blood; allergy; renal;
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 XX Key Misc-difference 10
 FT FT Misc-difference 13
 FT FT Misc-difference 13
 FT FT /label= unknown
 FT FT /label= unknown

XX WO9856804-A1.

XX 17-DEC-1998.

XX 11-JUN-1998; 98WO-US012125.

XX 13-JUN-1997; 97US-0049547P.

XX 13-JUN-1997; 97US-0049548P.

XX 13-JUN-1997; 97US-0049549P.

XX 13-JUN-1997; 97US-0049550P.

XX 13-JUN-1997; 97US-0049566P.

XX 13-JUN-1997; 97US-0049606P.

XX 13-JUN-1997; 97US-0049607P.

XX 13-JUN-1997; 97US-0049608P.

XX 13-JUN-1997; 97US-0049610P.

XX 13-JUN-1997; 97US-0049611P.

XX 13-JUN-1997; 97US-0050901P.

XX 13-JUN-1997; 97US-0052989P.

XX 08-JUL-1997; 97US-0051919P.

XX 18-AUG-1997; 97US-0055984P.

XX 12-SEP-1997; 97US-0058665P.

XX 12-SEP-1997; 97US-0058668P.

XX 12-SEP-1997; 97US-0058669P.

XX 12-SEP-1997; 97US-0058750P.

XX 12-SEP-1997; 97US-0058971P.

XX 12-SEP-1997; 97US-0058972P.

XX 12-SEP-1997; 97US-0058975P.

XX 02-OCT-1997; 97US-0060834P.

XX 02-OCT-1997; 97US-0060841P.

XX 02-OCT-1997; 97US-0060844P.

XX 02-OCT-1997; 97US-0060865P.

XX 02-OCT-1997; 97US-0061059P.

XX 02-OCT-1997; 97US-0061060P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Moore PA, Shi Y, Rosen CA, Ruben SM, Lafleur DW, Olsen HS;

XX Ebner R, Brewer LA, Young P, Greene JM, Ferrie AM, Yu G, Ni J;

XX Feng P;

XX N-PSDB; AAX04397.

XX WPI; 1999-080881/07.

XX New isolated human genes and the secreted polypeptides they encode -

XX useful for diagnosis and treatment of e.g. cancers, neurological

XX disorders, immune diseases, inflammation or blood disorders.

XX Claim 11; Page 313; 380pp; English.

XX This sequence represents a secreted human protein encoded by the gene

XX clone detailed in the descriptor line. The gene can be used to generate

XX fusion proteins by linking to the gene to a human immunoglobulin Fc

XX portion (e.g. AAX04302) for increasing the stability of the fused protein

XX as compared to the human protein only. The invention relates to 86 novel

XX genes and their fragments (nucleic acid sequences: AAX04311-X04410; amino

XX acid sequences AAW78126-W78225) which are useful for preventing, treating

XX or ameliorating medical conditions e.g. by protein or gene therapy. Also,

XX

CC pathological conditions can be diagnosed by determining the amount of the
 CC new polypeptides in a sample or by determining the presence of mutations
 CC in the new polynucleotides. Specific uses are described for each of the
 CC 86 polynucleotides, based on which tissues they are most highly expressed
 CC in (see AAX04311 for described uses)
 XX
 XX Sequence 13 AA;

Query Match 49.1%; Score 27; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVKT 8
 Db 5 FFVTTXLT 12

RESULT 9

ABP18094

ID ABP18094 standard; peptide; 11 AA.

XX AC ABP18094;

XX DT 11-SEP-2003 (revised)

XX DT 15-JUL-2002 (first entry)

XX DE HIV B58 super motif pol peptide #87.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

XX KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

XX KW vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US027765.

XX PR 05-OCT-1999; 99US-00412863.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

XX PT peptide groups, useful for vaccinating against HIV-1.

XX PS Claim 32; Page 239; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

XX sequence selected from 51 defined amino acid sequences (ABL25347 to

XX ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

XX be used for immunising subjects against HIV-1 infections. The use of

XX group-based vaccines has several advantages over traditional vaccines,

XX particularly when compared to the use of whole antigens in vaccine

XX compositions. There is evidence that the immune response to whole

XX antigens is directed largely toward variable regions of the antigen,

XX allowing for immune escape due to mutations. The groups for inclusion in

XX an group-based vaccine may be selected from conserved regions of viral or

XX tumour-associated antigens, which therefore reduces the likelihood of

XX escape mutants. Furthermore, immunosuppressive groups that may be present

XX in whole antigens can be avoided with the use of group-based vaccines. An

XX additional advantage of an group-based vaccine approach is the ability to

XX combine selected groups (CTL and HTL), and further, to modify the

XX composition of the groups, achieving, for example, enhanced

XX immunogenicity. Accordingly, the immune response can be modulated, as

XX appropriate, for the target disease. Similar engineering of the response

XX

CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
XX
SQ Sequence 11 AA;
Query Match 46.4%; Score 25.5; DB 4; Length 11;
Best Local Similarity 63.6%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 FFITTVKTA-W 10
| | | | |
Db 1 FTSTTVKACW 11

RESULT 10
ABP21178
ID ABP21178 standard; peptide; 9 AA.
XX
AC ABP21178;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif pol peptide #173.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 303; 449pp; English.

XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present

CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX
XX
SQ Sequence 9 AA;
Query Match 45.5%; Score 25; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
| | | | |
Db 1 FTSTTVKAA 9

RESULT 11
ABP13475
ID ABP13475 standard; peptide; 9 AA.
XX
AC ABP13475;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif pol peptide #390.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
FN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 144; 449pp; English.

XX
XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 9 AA;

Query Match 45.5%; Score 25; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
 | | | | | | |
 Db 1 FTSTTVKAA 9

RESULT 12
 AAU94469
 ID AAU94469 standard; peptide; 9 AA.
 XX AAU94469;
 AC
 CC
 CC
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CaTrF2E11 HLA binding peptide #202.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 XX WO200214361-A2.
 PN
 PD 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025782.
 PF
 PR 17-AUG-2000; 2000US-0226329P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 DR WPI; 2002-269179/31.
 XX
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX
 PS Example 11; Page 179; 270pp; English.

The invention relates to monitoring 83P2H3 (a calcium transport protein
 whose gene is located on chromosome 7q34) gene products in a biological
 sample from a patient who has or is suspected of having cancer
 (especially prostate cancer), comprises: (a) determining the status of
 83P2H3 gene products expressed by cells in a tissue sample from an
 individual and (b) comparing the status to the status of 83P2H3 gene
 products in a normal sample. Also included are modulators of 83P2H3
 function or status, generating antibodies/immune response against 83P2H3
 (or related protein CaTrF2E11 whose gene is located on chromosome
 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 derived from the protein, delivering a cytotoxic agent to a cell
 expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 recombinant protein comprising an antigen-binding region of the antibody,
 a non-human transgenic animal that produces the recombinant protein, a
 hybridoma that produces the recombinant protein, a single-chain
 monoclonal antibody that comprises the variable domains of the heavy and
 light chains of the anti-83P2H3 antibody, a vector comprising a
 polynucleotide that encodes the monoclonal antibody and inducing an
 immune response to a 83P2H3 protein, by providing a 83P2H3-related
 protein that comprises a T cell or B cell epitope, and contacting the
 epitope with an immune system T cell or B cell, respectively. The method
 is useful for monitoring 83P2H3 gene products in a biological sample for
 monitoring the presence of cancer in an individual. The modulator is
 useful for inhibiting the growth of cancer cells that express 83P2H3, for
 treating cancer and the vector is useful for treating a patient with a

cancer that expresses 83P2H3. The immunological methods are useful for
 generating an immune response against 83P2H3, and for detecting the
 presence of 83P2H3-related protein or polynucleotide in a biological
 sample from a patient who has or who is suspected of having cancer. The
 antibody is useful in prostate cancer diagnosis, prognosis, imaging
 methodologies and treatment, to detect and quantify 83P2H3 and mutant
 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 isolating 83P2H3 homologues/related molecules, and for generating anti-
 idiosyncratic antibodies that mimic the 83P2H3 protein. The present sequence
 is an HLA binding peptide motif from 83P2H3 or its related protein
 CaTrF2E11

XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 25; DB 5; Length 9;
 Best Local Similarity 57.1%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
 | | | | |
 Db 3 FFTTNIK 9

RESULT 13
 AAU94677
 ID AAU94677 standard; peptide; 9 AA.
 XX AAU94677;
 AC
 CC
 CC
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CaTrF2E11 HLA binding peptide #310.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 XX WO200214361-A2.
 PN
 PD 21-FEB-2002.
 XX
 XX 17-AUG-2001; 2001WO-US025782.
 PF
 PR 17-AUG-2000; 2000US-0226329P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 DR WPI; 2002-269179/31.
 XX
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX
 PS Example 11; Page 186; 270pp; English.

The invention relates to monitoring 83P2H3 (a calcium transport protein
 whose gene is located on chromosome 7q34) gene products in a biological
 sample from a patient who has or is suspected of having cancer
 (especially prostate cancer), comprises: (a) determining the status of
 83P2H3 gene products expressed by cells in a tissue sample from an
 individual and (b) comparing the status to the status of 83P2H3 gene
 products in a normal sample. Also included are modulators of 83P2H3
 function or status, generating antibodies/immune response against 83P2H3
 (or related protein CaTrF2E11 whose gene is located on chromosome
 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 derived from the protein, delivering a cytotoxic agent to a cell
 expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 recombinant protein comprising an antigen-binding region of the antibody,
 a non-human transgenic animal that produces the recombinant protein, a
 hybridoma that produces the recombinant protein, a single-chain
 monoclonal antibody that comprises the variable domains of the heavy and
 light chains of the anti-83P2H3 antibody, a vector comprising a
 polynucleotide that encodes the monoclonal antibody and inducing an
 immune response to a 83P2H3 protein, by providing a 83P2H3-related
 protein that comprises a T cell or B cell epitope, and contacting the
 epitope with an immune system T cell or B cell, respectively. The method
 is useful for monitoring 83P2H3 gene products in a biological sample for
 monitoring the presence of cancer in an individual. The modulator is
 useful for inhibiting the growth of cancer cells that express 83P2H3, for
 treating cancer and the vector is useful for treating a patient with a

CC a non-human transgenic animal that produces the recombinant protein, a
CC hybridoma that produces the recombinant protein, a single-chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83p2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83p2H3 protein, by providing a 83p2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83p2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83p2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83p2H3. The immunological methods are useful for
CC generating an immune response against 83p2H3, and for detecting the
CC presence of 83p2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83p2H3 and mutant
CC 83p2H3-related proteins, for purifying a 83p2H3-related protein, for
CC isolating 83p2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83p2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83p2H3 or its related protein
CC CaTrF2E11

XX SQ Sequence 9 AA;
Query Match 45.5%; Score 25; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 3 FFFTNIK 9

RESULT 14
AAU94889
ID AAU94889 standard; peptide; 9 AA.
AC AAU94889;
DT 02-JUL-2002 (first entry)
DE Human novel protein CaTrF2E11 HLA binding peptide #422.
XX Human; human leukocyte antigen; HLA; immunogen; 83p2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX Homo sapiens.
OS
XX WO200214361-A2.
PN
XX 21-FEB-2002.
PD
XX 17-AUG-2001; 2001WO-US025782.
PF
XX 17-AUG-2000; 2000US-0226329P.
PR
XX (AGEN-) AGENSYS INC.
PA
XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DBH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
DR
XX Monitoring 83p2H3 gene products for monitoring the presence of cancer in
PI a subject, comprises determining the status of 83p2H3 gene products in a
PT tissue sample from the subject and comparing it to a normal sample.
XX
XX Example 11; Page 194; 270pp; English.
PS
XX The invention relates to monitoring 83p2H3 (a calcium transport protein
XX CC

CC whose gene is located on chromosome 7q34) gene products in a biological
CC sample from a patient who has or is suspected of having cancer
CC (especially prostate cancer), comprises: (a) determining the status of
CC 83p2H3 gene products expressed by cells in a tissue sample from an
CC individual and (b) comparing the status to the status of 83p2H3 gene
CC products in a normal sample. Also included are modulators of 83p2H3
CC function or status, generating antibodies/immune response against 83p2H3
CC (or related protein CaTrF2E11 whose gene is located on chromosome
CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
CC derived from the protein, delivering a cytotoxic agent to a cell
CC recombinant protein comprising an antigen-binding region of the antibody,
CC hybridoma that produces the recombinant protein, a single-chain
CC monoclonal antibody that comprises the variable domains of the heavy and
CC light chains of the anti-83p2H3 antibody, a vector comprising a
CC polynucleotide that encodes the monoclonal antibody and inducing an
CC immune response to a 83p2H3 protein, by providing a 83p2H3-related
CC protein that comprises a T cell or B cell epitope, and contacting the
CC epitope with an immune system T cell or B cell, respectively. The method
CC is useful for monitoring 83p2H3 gene products in a biological sample for
CC monitoring the presence of cancer in an individual. The modulator is
CC useful for inhibiting the growth of cancer cells that express 83p2H3, for
CC treating cancer and the vector is useful for treating a patient with a
CC cancer that expresses 83p2H3. The immunological methods are useful for
CC generating an immune response against 83p2H3, and for detecting the
CC presence of 83p2H3-related protein or polynucleotide in a biological
CC sample from a patient who has or who is suspected of having cancer. The
CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
CC methodologies and treatment, to detect and quantify 83p2H3 and mutant
CC 83p2H3-related proteins, for purifying a 83p2H3-related protein, for
CC isolating 83p2H3 homologues/related molecules, and for generating anti-
CC idiotype antibodies that mimic the 83p2H3 protein. The present sequence
CC is an HLA binding peptide motif from 83p2H3 or its related protein
CC CaTrF2E11

XX SQ Sequence 9 AA;
Query Match 45.5%; Score 25; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 1 FFFTNIK 7

RESULT 15
ABP21186
ID ABP21186 standard; peptide; 10 AA.
XX
AC ABP21186;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
XX HIV A03 motif pol peptide #181.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
KW vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus 1.
OS
XX WO200124810-A1.
PN
XX 12-APR-2001.
PD
XX 05-OCT-2000; 2000WO-US027766.
PF
XX 05-OCT-1999; 99US-00412863.
PR
XX (EPIM-) EPIMMUNE INC.
PA

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 DR WPI; 2001-354887/37.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT Claim 32; Page 303; 448pp; English.
 PS
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX Sequence 10 AA;
 SQ

Query Match 45.5%; Score 25; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
 Db 2 FTSTTVKAA 10
 | | | | |
 1 1 1 1 1 1 1 1 1 1
 2 1 1 1 1 1 1 1 1 1

RESULT 16
 ABP11874
 ID ABP11874 standard; peptide; 10 AA.
 XX
 AC ABP11874;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A01 super motif pol peptide #146.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT Claim 32; Page 112; 448pp; English.
 PS
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX Sequence 10 AA;
 SQ

Query Match 45.5%; Score 25; DB 4; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 FFITTVKTA 9
 Db 1 FTSTTVKAA 9
 | | | | |
 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 1 1 1

RESULT 17
 ABP16363
 ID ABP16363 standard; peptide; 10 AA.
 XX
 AC ABP16363;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A24 super motif pol peptide #543.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

CC protein complex is a regulatory protein, which regulates the specificity
 CC of the channel forming protein for nucleic acid transport. Human
 CC cytosolic malate dehydrogenase (CMDH; A047750) was used as the second
 CC subunit protein in the invention. The protein complex is useful for
 CC reducing nucleic acid toxicity in kidney cells, and for facilitating the
 CC transport of nucleic acids into cells for a number of therapeutic
 CC applications. The present sequence is a p36 tryptic peptide, which was
 CC used in a sequence homology alignment with CMDH (given in Figure 3)
 XX
 SQ Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 83.3%; Pred. No. 6.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 FITTVK 7
 Db 3 FITTVQ 8
 |||||:

RESULT 20
 ABG98537
 ID ABG98537 standard; peptide; 10 AA.

XX AC ABG98537;

XX DT 13-JAN-2003 (first entry)

XX DE F protein decapeptide #24.

XX F protein; RSV; decapeptide; negative sense single stranded RNA virus;
 KW viral F protein; F protein mediated host cell virion fusion; virucide;
 KW F protein mediated host cell virion budding.

XX OS Respiratory syncytial virus.

XX PN WO200242326-A1.

XX PD 30-MAY-2002.

XX PF 22-NOV-2001; 2001WO-AU001517.

XX PR 22-NOV-2000; 2000US-0252767P.

XX PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.

XX PI Mason AJ, Tucker SP, Young PR;

XX DR WPI; 2002-599372/64.

XX PT Facilitating production of a protein for analyzing, designing and/or
 PT modifying an agent that can interact with a viral F protein, comprises
 PT expressing a nucleic acid optimized for expression of the protein, using
 PT a eukaryotic cell.

XX PS Claim 42; Page 100; 367pp; English.

XX The invention relates to a method for facilitating production of a
 CC protein or its derivative from a negative sense single stranded RNA
 CC virus, by expressing a nucleic acid molecule encoding the protein in a
 CC host cell, where the nucleic acid is optimised for expression by a
 CC eukaryotic cell. The protein, especially F protein, is useful for
 CC analysing, designing and/or modifying an agent capable of interacting
 CC with a viral F protein or its derivative and modulating a functional
 CC activity associated with the protein, by contacting the protein with a
 CC putative agent and assessing the degree of interactive complementarity of
 CC the agent with the protein. An optimised nucleic acid or its derivative,
 CC equivalent, analogue or mimetic is useful for interacting with a viral F
 CC protein and modulating a functional activity associated with the viral
 CC protein, for use in the manufacture of a medicament utilised in the
 CC therapeutic and/or prophylactic treatment of conditions characterised by
 CC infection with a negative sense single stranded RNA virus, and for
 CC modulating a functional activity associated with a viral F protein in a

CC subject, preferably a mammal, especially a human, where the functional
 CC activity is F protein mediated host cell virion fusion and/or virion
 CC budding and the modulating is down regulation. Sequences ABG98514-
 CC ABG99058 represent F protein decapeptides of the invention
 XX
 SQ Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 22.2%; Pred. No. 6.1e+02;
 Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 FITTVKTAW 10
 Db 1 YLSALRTGW 9
 ::::|

RESULT 21
 ABG98536
 ID ABG98536 standard; peptide; 10 AA.

XX AC ABG98536;

XX DT 13-JAN-2003 (first entry)

XX DE F protein decapeptide #23.

XX F protein; RSV; decapeptide; negative sense single stranded RNA virus;
 KW viral F protein; F protein mediated host cell virion fusion; virucide;
 KW F protein mediated host cell virion budding.

XX OS Respiratory syncytial virus.

XX PN WO200242326-A1.

XX PD 30-MAY-2002.

XX PF 22-NOV-2001; 2001WO-AU001517.

XX PR 22-NOV-2000; 2000US-0252767P.

XX PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.

XX PI Mason AJ, Tucker SP, Young PR;

XX DR WPI; 2002-599372/64.

XX PT Facilitating production of a protein for analyzing, designing and/or
 PT modifying an agent that can interact with a viral F protein, comprises
 PT expressing a nucleic acid optimized for expression of the protein, using
 PT a eukaryotic cell.

XX PS Claim 42; Page 100; 367pp; English.

XX The invention relates to a method for facilitating production of a
 CC protein or its derivative from a negative sense single stranded RNA
 CC virus, by expressing a nucleic acid molecule encoding the protein in a
 CC host cell, where the nucleic acid is optimised for expression by a
 CC eukaryotic cell. The protein, especially F protein, is useful for
 CC analysing, designing and/or modifying an agent capable of interacting
 CC with a viral F protein or its derivative and modulating a functional
 CC activity associated with the protein, by contacting the protein with a
 CC putative agent and assessing the degree of interactive complementarity of
 CC the agent with the protein. An optimised nucleic acid or its derivative,
 CC equivalent, analogue or mimetic is useful for interacting with a viral F
 CC protein and modulating a functional activity associated with the viral
 CC protein, for use in the manufacture of a medicament utilised in the
 CC therapeutic and/or prophylactic treatment of conditions characterised by
 CC infection with a negative sense single stranded RNA virus, and for
 CC modulating a functional activity associated with a viral F protein in a
 CC subject, preferably a mammal, especially a human, where the functional
 CC activity is F protein mediated host cell virion fusion and/or virion
 CC budding and the modulating is down regulation. Sequences ABG98514-
 CC ABG99058 represent F protein decapeptides of the invention

XX SQ Sequence 10 AA;
 Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 22.2%; Pred. No. 6.1e+02;
 Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 2 FITVKTAW 10
 : : : : :
 Db 2 YLSALRTGW 10
 : : : : :
 RESULT 22
 AAU95405
 ID AAU95405 standard; peptide; 10 AA.
 XX
 AC AAU95405;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CaTrF2E11 HLA binding peptide #672.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 PN WO200214361-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025782.
 XX
 PR 17-AUG-2000; 2000US-0226329P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX
 WPI; 2002-269179/31.
 XX
 PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX
 PS Example 11; Page 197; 270pp; English.
 XX
 CC The invention relates to monitoring 83P2H3 (a calcium transport protein
 CC whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer.
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC immunologic response to a 83P2H3 protein, by providing a 83P2H3-related
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for

CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CaTrF2E11
 XX
 SQ Sequence 10 AA;
 Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 57.1%; Pred. No. 6.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FFITTVK 7
 : : : : :
 Db 1 FFFTNIK 7
 : : : : :
 RESULT 23
 AAU94768
 ID AAU94768 standard; peptide; 10 AA.
 XX
 AC AAU94768;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human novel protein CaTrF2E11 HLA binding peptide #351.
 XX
 KW Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
 KW calcium transport protein; cancer; prostate cancer; cytostatic;
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
 XX
 OS Homo sapiens.
 XX
 PN WO200214361-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025782.
 XX
 PR 17-AUG-2000; 2000US-0226329P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX
 WPI; 2002-269179/31.
 XX
 PT Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX
 PS Example 11; Page 189; 270pp; English.
 XX
 CC The invention relates to monitoring 83P2H3 (a calcium transport protein
 CC whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein CaTrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC immunologic response to a 83P2H3 protein, by providing a 83P2H3-related
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell, respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for

recombinant protein comprising an antigen-binding region of the antibody, a non-human transgenic animal that produces the recombinant protein, a monoclonal antibody that comprises the variable domains of the heavy and light chains of the anti-83P2H3 antibody, a vector comprising a polynucleotide that encodes the monoclonal antibody and inducing an immune response to a 83P2H3 protein, by providing a 83P2H3-related protein that comprises a T cell or B cell epitope, and contacting the epitope with an immune system T cell or B cell, respectively. The method is useful for monitoring 83P2H3 gene products in a biological sample for monitoring the presence of cancer in an individual. The modulator is useful for inhibiting the growth of cancer cells that express 83P2H3, for treating cancer and the vector is useful for treating a patient with a cancer that expresses 83P2H3. The immunological methods are useful for generating an immune response against 83P2H3, and for detecting the presence of 83P2H3-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The antibody is useful in prostate cancer diagnosis, prognosis, imaging 83P2H3-related proteins, for purifying a 83P2H3-related protein, for isolating 83P2H3 homologues/related molecules, and for generating anti-idiotypic antibodies that mimic the 83P2H3 protein. The present sequence is an HLA binding peptide motif from 83P2H3 or its related protein CaTrF2E11

Sequence 10 AA;
Query Match 45.5%; Score 25; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 4 FFTNIK 10

RESULT 24
AAU94575
ID AAU94575 standard; peptide; 10 AA.
AC AAU94575;

XX 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #258.
DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX Homo sapiens.

XX WO200214361-A2.
XX 21-FEB-2002.
XX 17-AUG-2001; 2001WO-US025782.
XX 17-AUG-2000; 2000US-0226329P.
XX (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;
PI Levin E, Hubert RS, Ge W, Jakobovits A;
XX WPI; 2002-269179/31.
XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample.

XX Example 11; Page 182; 270pp; English.
XX

The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological sample from a patient who has or is suspected of having cancer (especially prostate cancer), comprises: (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 function or status, generating antibodies/immune response against 83P2H3 (or related protein CaTrF2E11 whose gene is located on chromosome 12q24.1) using identified HLA (human leukocyte antigen) binding peptides derived from the protein, delivering a cytotoxic agent to a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a recombinant protein comprising an antigen-binding region of the antibody, a non-human transgenic animal that produces the recombinant protein, a monoclonal antibody that produces the recombinant protein, a single-chain light chains of the anti-83P2H3 antibody, a vector comprising a polynucleotide that encodes the monoclonal antibody and inducing an immune response to a 83P2H3 protein, by providing a 83P2H3-related protein that comprises a T cell or B cell epitope, and contacting the epitope with an immune system T cell or B cell, respectively. The method is useful for monitoring 83P2H3 gene products in a biological sample for monitoring the presence of cancer in an individual. The modulator is useful for inhibiting the growth of cancer cells that express 83P2H3, for treating cancer and the vector is useful for treating a patient with a cancer that expresses 83P2H3. The immunological methods are useful for generating an immune response against 83P2H3, and for detecting the presence of 83P2H3-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The antibody is useful in prostate cancer diagnosis, prognosis, imaging 83P2H3-related proteins, for purifying a 83P2H3-related protein, for isolating 83P2H3 homologues/related molecules, and for generating anti-idiotypic antibodies that mimic the 83P2H3 protein. The present sequence is an HLA binding peptide motif from 83P2H3 or its related protein CaTrF2E11

Sequence 10 AA;

Query Match 45.5%; Score 25; DB 5; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
||| :|
Db 4 FFTNIK 10

RESULT 25
AAU95402
ID AAU95402 standard; peptide; 10 AA.
AC AAU95402;

XX 02-JUL-2002 (first entry)
XX Human novel protein CaTrF2E11 HLA binding peptide #669.
DE Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2E11;
KW calcium transport protein; cancer; prostate cancer; cytostatic;
KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.
XX Homo sapiens.

XX WO200214361-A2.
XX 21-FEB-2002.
XX 17-AUG-2001; 2001WO-US025782.
XX 17-AUG-2000; 2000US-0226329P.
XX (AGEN-) AGENSYS INC.
PA

XX Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH;
 PI Levin E, Hubert RS, Ge W, Jakobovits A;
 XX WPI; 2002-269179/31.
 XX Monitoring 83P2H3 gene products for monitoring the presence of cancer in
 PT a subject, comprises determining the status of 83P2H3 gene products in a
 PT tissue sample from the subject and comparing it to a normal sample.
 XX Example 11; Page 197; 270pp; English.
 PS The invention relates to monitoring 83P2H3 (a calcium transport protein
 XX whose gene is located on chromosome 7q34) gene products in a biological
 CC sample from a patient who has or is suspected of having cancer
 CC (especially prostate cancer), comprises: (a) determining the status of
 CC 83P2H3 gene products expressed by cells in a tissue sample from an
 CC individual and (b) comparing the status to the status of 83P2H3 gene
 CC products in a normal sample. Also included are modulators of 83P2H3
 CC function or status, generating antibodies/immune response against 83P2H3
 CC (or related protein CatrF2E11 whose gene is located on chromosome
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding peptides
 CC derived from the protein, delivering a cytotoxic agent to a cell
 CC expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a
 CC recombinant protein comprising an antigen-binding region of the antibody,
 CC a non-human transgenic animal that produces the recombinant protein, a
 CC hybridoma that produces the recombinant protein, a single-chain
 CC monoclonal antibody that comprises the variable domains of the heavy and
 CC light chains of the anti-83P2H3 antibody, a vector comprising a
 CC polynucleotide that encodes the monoclonal antibody and inducing an
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related
 CC protein that comprises a T cell or B cell epitope, and contacting the
 CC epitope with an immune system T cell or B cell respectively. The method
 CC is useful for monitoring 83P2H3 gene products in a biological sample for
 CC monitoring the presence of cancer in an individual. The modulator is
 CC useful for inhibiting the growth of cancer cells that express 83P2H3, for
 CC treating cancer and the vector is useful for treating a patient with a
 CC cancer that expresses 83P2H3. The immunological methods are useful for
 CC generating an immune response against 83P2H3, and for detecting the
 CC presence of 83P2H3-related protein or polynucleotide in a biological
 CC sample from a patient who has or who is suspected of having cancer. The
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-
 CC idiotypic antibodies that mimic the 83P2H3 protein. The present sequence
 CC is an HLA binding peptide motif from 83P2H3 or its related protein
 CC CatrF2E11
 XX CatrF2E11
 SQ Sequence 10 AA;
 Query Match 45.5%; Score 25; DB 5; Length 10;
 Best Local Similarity 57.1%; Pred. No. 6.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 OY 1 FFTTVK 7
 DB 2 FFTNIX 8
 RESULT 26
 ADC44696
 ID ADC44696 standard; peptide; 12 AA.
 XX AC ADC44696;
 XX 18-DEC-2003 (first entry)
 DT Endothelial cell binding peptide SEQ ID NO:425.
 DE endothelial cell binding protein; ECP; anti-tumour; cytostatic;
 XX vasotrophic; antiproliferative; dermatological; ophthalmological;
 KW antidiabetic; antiarthritic; vulnary; antiulcer; antiinflammatory;
 XX CatrF2E11

KW antibacterial; gynaecological; angiogenesis.
 XX Synthetic.
 OS WO2003037172-A2.
 XX 08-MAY-2003.
 PD 01-NOV-2002; 2002WO-US035258.
 PF 01-NOV-2001; 2001US-0334822P.
 PR (GPCB-) GPC BIOTECH INC.
 XX Gyuris J, Lamphere L, Morris AJ, Tsaioun K;
 PI WPI; 2003-482072/45.
 XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
 DR proliferation and/or migration of endothelial cells, and for modulating
 PT angiogenesis, has endothelial cell binding protein sequences.
 PT Claim 3; SEQ ID NO 425; 126pp; English.
 XX The invention relates to a novel isolated, synthetic or recombinant
 CC peptide or polypeptide which includes one or more endothelial cell
 CC binding protein (ECP) sequences. A peptide of the invention has anti-
 CC tumour, cytostatic, vasotrophic, antiproliferative, dermatological,
 CC ophthalmological, antidiabetic, antiarthritic, vulnary, antiulcer,
 CC antinflammatory, antibacterial, and gynaecological activity. The peptide
 CC is useful for promoting, reducing the proliferation and/or migration of
 CC endothelial cells, by treating the cells with an ECP agonist, which is
 CC preferably the peptide, to promote proliferation and/or migration of the
 CC treated cells, and for reducing or promoting angiogenesis, by treating
 CC the cells with an ECP antagonist, which is preferably the peptide of the
 CC invention. A peptide of the invention is also useful for manufacturing a
 CC medicament for promoting angiogenesis, by admixing an ECP agonist or
 CC ECP antagonist to promote or reduce angiogenesis at one or more sites in
 CC a treated mammal. The medicament is useful for promoting or reducing
 CC angiogenesis. ECP sequences are useful to alter the infectivity spectrum
 CC of a viral particle. The present sequence represents an ECP of the
 CC invention.
 XX Sequence 12 AA;
 Query Match 45.5%; Score 25; DB 7; Length 12;
 Best Local Similarity 66.7%; Pred. No. 7.3e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 TVKTAW 10
 DB 1 TVKAGW 6
 RESULT 27
 AAB38906
 ID AAB38906 standard; peptide; 13 AA.
 XX AC AAB38906;
 XX 02-FEB-2001 (first entry)
 DT HIV-1 peptide epitope #259.
 DE Vaccine; anti-HIV; HIV envelope protein; HIV infection.
 KW Human immunodeficiency virus.
 XX WO200058438-A2.
 PN 05-OCT-2000.
 PD 29-MAR-2000; 2000WO-US008232.
 PF

XX 29-MAR-1999; 99US-0126938P.
 XX (BERN/) BERNSTEIN D.
 XX (CHOW/) CHOWDHURY A.
 XX (KOZH/) KOZHICH A.
 XX (MOTS/) MOTSENBOCKER M.
 XX Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
 XX WPI; 2000-656164/63.
 XX Synthetic peptides useful for preventing and treating HIV infection in
 XX mammals, comprising a conformationally constrained portion and a portion
 XX with continuous stretch of amino acids of predicted secondary structure.
 XX Disclosure; Page 26; 69pp; English.
 XX The present invention relates to peptides (AAB38648-B38970) comprising a
 XX first conformationally constrained portion with a cross-linked group of a
 XX HIV envelope protein that induces neutralising antibodies, and a second
 XX portion comprising a continuous stretch of at least 5 amino acids having
 XX a predicted secondary structure. The present sequence is one such
 XX peptide. The peptides of the present invention are useful as a vaccine
 XX for prophylactic or therapeutic treatment of a mammal for HIV infection
 XX Sequence 13 AA;
 XX
 XX Query Match 45.5%; Score 25; DB 3; Length 13;
 XX Best Local Similarity 66.7%; Pred. No. 7.9e+02;
 XX Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 XX
 XX QY 4 TTVK--TAW 10
 XX ||||| :|
 XX 3 TTVKWNWSW 11
 XX
 XX RESULT 28
 XX AAB38842
 XX ID AAB38842 standard; peptide; 13 AA.
 XX AC AAB38842;
 XX XX 02-FEB-2001 (first entry)
 XX DT HIV-1 peptide epitope #195.
 XX DE Vaccine; anti-HIV; HIV envelope protein; HIV infection.
 XX KW Human immunodeficiency virus.
 XX OS WO200058438-A2.
 XX PN 05-OCT-2000.
 XX PD 29-MAR-2000; 2000WO-US008232.
 XX PF 29-MAR-1999; 99US-0126938P.
 XX PR (BERN/) BERNSTEIN D.
 XX PA (CHOW/) CHOWDHURY A.
 XX PA (KOZH/) KOZHICH A.
 XX PA (MOTS/) MOTSENBOCKER M.
 XX PI Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
 XX WPI; 2000-656164/63.
 XX Synthetic peptides useful for preventing and treating HIV infection in
 XX mammals, comprising a conformationally constrained portion and a portion
 XX with continuous stretch of amino acids of predicted secondary structure.
 XX Disclosure; Page 24; 69pp; English.

XX The present invention relates to peptides (AAB38648-B38970) comprising a
 XX first conformationally constrained portion with a cross-linked group of a
 XX HIV envelope protein that induces neutralising antibodies, and a second
 XX portion comprising a continuous stretch of at least 5 amino acids having
 XX a predicted secondary structure. The present sequence is one such
 XX peptide. The peptides of the present invention are useful as a vaccine
 XX for prophylactic or therapeutic treatment of a mammal for HIV infection
 XX Sequence 13 AA;
 XX
 XX Query Match 45.5%; Score 25; DB 3; Length 13;
 XX Best Local Similarity 66.7%; Pred. No. 7.9e+02;
 XX Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 XX
 XX QY 4 TTVK--TAW 10
 XX ||||| :|
 XX 3 TTVKWNWSW 11
 XX
 XX RESULT 29
 XX AAR79122
 XX ID AAR79122 standard; peptide; 10 AA.
 XX AC AAR79122;
 XX XX 27-AUG-2003 (revised)
 XX DT 21-FEB-1996 (first entry)
 XX DE Algal lectin N-terminal with unique sugar-chain binding specificity.
 XX KW Algae; lectin; sugar; carbohydrate; specificity; diagnosis; therapy;
 XX KW cancer; immunomodulator; transplant rejection; autoimmune disease.
 XX OS Eucheuma sp.
 XX PN WO9518149-A1.
 XX XX 06-JUL-1995.
 XX PF 19-DEC-1994; 94WO-JP002140.
 XX PR 24-DEC-1993; 93JP-00328218.
 XX XX (MARI-) MARINE GREENS LAB CO LTD.
 XX PA Kawakubo A, Makino H, Ninomiya M, Bitou N;
 XX WPI; 1995-246334/32.
 XX PT Algal lectin with unique sugar-chain binding specificity - deriv. from
 XX Eucheuma or Kappaphycus species, is useful for diagnosis and therapy of
 XX cancer and immune disorders.
 XX PS Claim 1; Page 21; 38pp; Japanese.
 XX AAR79121 and AAR79122 are possible N-terminal peptides from a new algal
 XX lectin which are derived from the Eucheuma species of alga. More
 XX specifically the lectin is derived from either E. serria, E. cottonii,
 XX E. gelatinosa or E. amakusaensis. The N-terminal peptides obey the general
 XX formula G-R-Y-T-V-X-N-Q-W-G where X= Q or K. The lectins have a unique
 XX ability to bind specifically to certain sugar-chains, and bind
 XX specifically to fetuin, asialofetuin, thyroglobulin and yeast mannan. The
 XX lectin may be used in a variety of ways; as an immunomodulator, as a
 XX diagnostic and test reagent, as a specific adsorbent for separation and
 XX analysis of sugars, as an organ transplant rejection inhibitor, as an
 XX anticancer agent, for the treatment of autoimmune disease and as a
 XX lymphocyte growth factor. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 10 AA;
 XX
 XX Query Match 43.6%; Score 24; DB 2; Length 10;
 XX Best Local Similarity 66.7%; Pred. No. 9.1e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
|||
Db 4 TVKNQW 9

RESULT 30
AAW09941
ID AAW09941 standard; protein; 10 AA.
XX AC AAW09941;
XX XX
XX 13-MAR-1998 (first entry)
XX DE Peptide from clone 11 from cell intrusion experiment.
XX KW Fusion protein; surface; bacterial cell; peptide library; aggregate;
XX KW screening; diagnosis; treatment; autoimmune disease; cancer.
XX OS Synthetic.
XX XX
XX PN W09706264-Al.
XX XX
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-UP002196.
XX XX
XX PR 04-AUG-1995; 95JP-00199745.
XX XX (SUME) SUMITOMO ELECTRIC IND CO.
XX PI Shimbara N, Saya H;
XX XX
XX DR WPI; 1997-154269/14.
XX DR N-PSDB; AAT66417.
XX XX
XX PT Bacterial peptide library expressing cell invasive protein on the cell
XX PT surface - bonded to a random target protein which is thus introduced to
XX PT target cells.
XX PS Disclosure; Page 45; 86pp; Japanese.
XX XX
XX CC Escherichia coli was introduced into VAL3 to obtain a cell intrusion E.
XX CC coli. This was carried out using ESPER. 22 clones were selected from this
XX CC and plasmid extracted. DNA sequencing was carried out by Taq cycle
XX CC sequencing. The invention concerns a fusion protein which presents at the
XX CC surface of bacterial cells transformed with DNA coding for the fusion
XX CC protein. Bacterium exhibiting the fused protein on its surface are used
XX CC to produce a bacterial peptide library which is an aggregate of such
XX CC bacteria. The bacterial peptide library is useful in identification of
XX CC target proteins having a desired biochemical activity in target cells,
XX CC for diagnosis or treatment of diseases such as autoimmune diseases and
XX CC cancer. The bacterial library readily reproduces and is relatively
XX CC stable, without significant change or denaturation during preservation
XX SQ Sequence 10 AA;

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 TVKTAW 10
|:|:|
Db 1 TNRFTW 6

RESULT 31
AAG86162
ID AAG86162 standard; peptide; 10 AA.
XX AC AAG86162;
XX XX

DT 11-SEP-2001 (first entry)
XX XX
XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1111.
XX XX
XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX KW drug discovery; drug design.
XX OS
XX OS Saccharomyces cerevisiae.
XX XX
XX PN W0200142276-Al.
XX XX
XX PD 14-JUN-2001.
XX XX
XX PF 13-DEC-2000; 2000WO-CB004773.
XX XX
XX PR 13-DEC-1999; 99GB-00029471.
XX XX (PROT-) PROTEOM LTD.
XX PA
XX PI Roberts GW, Heal JR;
XX XX
XX DR WPI; 2001-367863/38.
XX XX
XX XX Identifying complementary peptides by analysis of protein and nucleotide
XX PT sequence databases, useful in drug design.
XX PT
XX PS Example 3; Page 183; 488pp; English.
XX XX
XX CC The invention relates to the identification of complementary peptides by
XX CC analysis of protein and nucleotide sequence databases from higher
XX CC eukaryotic genomes, excluding human and plants. The specific
XX CC complementary peptides interact with their relevant target proteins
XX CC encoded in the eukaryote genome. The peptides may be used as reagents and
XX CC drugs for drug discovery and as lead ligands for drug design and
XX CC development. The present sequence is a complementary peptide from
XX CC Saccharomyces cerevisiae
XX SQ Sequence 10 AA;

Query Match 43.6%; Score 24; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
|||
Db 2 VKAAW 6

RESULT 32
AAW21219
ID AAW21219 standard; peptide; 11 AA.
XX XX
XX AC AAW21219;
XX XX
XX DT 29-JUL-1997 (first entry)
XX XX
XX XX Farnesyl synthetase derived signal oligopeptide #19.
XX XX
XX KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; STV;
XX KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
XX KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
XX KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
XX KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
XX KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
XX KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
XX KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
XX KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
XX KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
XX KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
XX OS Homo sapiens.
XX XX
XX XX W09519568-Al.

PA (BIOA-) INST BIOANALYTIK GEMEINNUTZIGE GMBH.
 XX Skerra A, Schmidt T;
 XX WPI; 1994-153484/19.
 DR N-PSDB; AAQ62672.
 XX New fusion peptide(s) - have easily controlled binding properties and are
 PT capable of binding to streptavidin.
 XX Disclosure; Page 11; 53pp; English.
 XX

CC Six derivatives of pASK46 (a plasmid for expression of the D1.3Fv
 fragment in E.coli) were produced which encode 4 different peptides at
 the C-terminus of VH and 2 peptides at the C-terminus of VL of the D1.3Fv
 fragment. The peptides fused to the C-terminus are all examples of
 streptavidin-binding peptides corresponding to a generic formula (see
 AARS2698). The peptides do not interfere with the protein function but
 facilitate purification by conferring streptavidin-binding properties on
 the fusion protein
 XX Sequence 12 AA;
 SQ

Query Match 43.6%; Score 24; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VKTAW 10
 Db :|||
 1 IKSAAW 5

RESULT 35
 AARS2696
 ID AARS2696 standard; protein; 12 AA.
 XX
 AC AARS2696;
 XX
 DT 10-JAN-1995 (first entry)
 XX
 DE pASK46-pl11L encoded C-terminal streptavidin-binding sequence.
 XX Streptavidin binding peptide; fusion protein; immunoglobulin; Ig;
 KW light chain variable region; affinity chromatography; purification;
 KW peptide tag.
 XX Synthetic.
 OS
 XX

FH Key Location/Qualifiers
 FT Peptide 5..12
 FT /note= "streptavidin-binding octapeptide fused to C-terminus of VL chain"
 XX
 XX GB2272698-A.
 XX
 XX 25-MAY-1994.
 XX
 XX 01-NOV-1993; 93GB-00022501.
 XX
 XX 03-NOV-1992; 92DE-04237113.
 XX

PA (BIOA-) INST BIOANALYTIK GEMEINNUTZIGE GMBH.
 XX Skerra A, Schmidt T;
 XX WPI; 1994-153484/19.
 DR N-PSDB; AAQ62671.
 XX New fusion peptide(s) - have easily controlled binding properties and are
 PT capable of binding to streptavidin.
 XX Disclosure; Page 11; 53pp; English.
 XX

CC Six derivatives of pASK46 (a plasmid for expression of the D1.3Fv
 fragment in E.coli) were produced which encode 4 different peptides at
 the C-terminus of VH and 2 peptides at the C-terminus of VL of the D1.3Fv
 fragment. The peptides fused to the C-terminus are all examples of
 streptavidin-binding peptides corresponding to a generic formula (see
 AARS2698). The peptides do not interfere with the protein function but
 facilitate purification by conferring streptavidin-binding properties on
 the fusion protein
 XX Sequence 12 AA;
 SQ

Query Match 43.6%; Score 24; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 6 VKTAW 10
 Db :|||
 1 IKSAAW 5

RESULT 36
 ABP9066
 ID ABP9066 standard; peptide; 12 AA.
 XX
 AC ABP9066;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 DE ErbB2 cell overexpression EOP1-88 peptide SEQ ID NO:103.
 XX
 KW ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;
 KW EOP1; EOP; ErbB2 overexpression feature; cytostatic; vaccine;
 KW gene therapy.
 XX Homo sapiens.
 OS
 XX WO200290991-A2.
 XX
 XX 14-NOV-2002.
 XX
 XX 02-MAY-2001; 2002WO-CB002047.
 XX
 XX 03-MAY-2001; 2001GB-00010886.
 PR 23-NOV-2001; 2001GB-00028183.
 XX
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 XX Herath HMC, Page MJ;
 PI WPI; 2003-103531/09.
 XX
 XX Diagnosing and treating ErbB2-related cancer, comprises generating ErbB2
 Overexpression Features (EOPs) from test samples from a subject by
 electrophoresis, and comparing the EOPs in the sample with a
 predetermined reference range.
 XX
 XX Claim 3; Page 20; 106pp; English.
 XX
 XX The present invention describes a method for screening or diagnosing
 ErbB2-related cancer. The method comprises generating ErbB2
 overexpression features (EOPs) from test samples of body fluid from the
 subject by electrophoresis, and comparing the EOPs in the test sample
 with that from normal subjects or with an expression reference feature
 (ERF) in the test sample. Also described: (1) an antibody capable of
 immunospecific binding to an ErbB2 overexpression protein isoform (EOP1);
 (2) pharmaceutical compositions comprising an EOP1, a nucleic acid
 encoding an EOP1, an amount of the above antibody or its fragment, and a
 carrier; (3) a kit comprising one or more antibodies and/or EOPs cited
 above, other reagents and instructions for use; (4) methods of treating
 or preventing ErbB2-related cancer; (5) methods of screening for or
 identifying agents that interact with or modulate the expression or
 activity of one or more EOPs, EOP1 fragment, EOP1-related polypeptides,
 or EOP1-fusion proteins; (6) a method for modulating the activity of one

CC or more of the ErbB2 EOPIS, comprising administering to a subject an
CC agent identified by the method of (5); and (7) a method for identifying
CC targets for therapeutic modulation of ErbB2-related cancer. EOPIS have
CC cytosolic activity and can be used in vaccines and gene therapy. The
CC method is useful in screening, diagnosing, preventing or treating ErbB2-
CC related cancer, determining the stage or severity of ErbB2-related
CC cancer, identifying a subject at risk of developing ErbB2-related cancer,
CC monitoring the effect of therapy administered to a subject with ErbB2-
CC related cancer, and for drug screening or drug development. The kit is
CC useful in carrying out the above methods. ABP98940 to ABP99206 represent
CC specifically claimed EOPIS from the present invention
XX
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PFITTVKVT 8
| : ||| |
Db 4 FTLTVDVT 11

RESULT 37
ABU14354
ID ABU14354 standard; peptide; 12 AA.

XX AC ABU14354;

XX DT 12-MAR-2003 (first entry)

XX DE C- or N-terminal cysteine containing hFSH peptide #100.

XX KW Biomolecule detection; pixel array; micro-array support;
XX KW molecule binding; binding molecule; support surface; surface patch;
XX KW high density arraying; enzyme-linked-assay; hFSH;
XX KW human follicle-stimulating hormone.

XX OS Homo sapiens.

XX PN WO200266984-A2.

XX PD 29-AUG-2002.

XX PF 15-FEB-2002; 2002WO-NL000097.

XX PR 16-FEB-2001; 2001EP-00200551.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Puijk WC, Van Dijk E, Slootstra JW;

XX DR WPI; 2003-103161/09.

XX PT Novel support used for micro-arrays and its use in detection of (bio)
XX PT molecules.

XX PS Example 3; Fig 6C; 4lpp; English.

XX CC The present invention relates to a method for the detection of
XX CC biomolecules in pixel arrays and the supports used for the micro-arrays.
XX CC The novel supports for the micro-arrays are suitable for determining the
XX CC binding of a first member molecule within a library of spots of tentative
XX CC first member binding molecules with a second member binding molecule. The
XX CC support is provided with a support surface where surface patches are
XX CC interspersed with surface areas that are materially distinct from the
XX CC patches. The support and method of the invention are useful for
XX CC identifying or obtaining a synthetic molecule comprising a binding site,
XX CC or a binding molecule capable of binding to a binding site. The molecule
XX CC is useful for interfering with, or effecting binding to a binding
XX CC molecule. The novel support for a micro-array and the method provide high
XX CC density arraying (testing many binding events in one go) and enzyme-
XX CC linked-assays (very sensitive) allowing the detection of more binding

CC pairs more rapidly. ABU14255-ABU14437 represent human follicle-
CC stimulating hormone (hFSH) derived peptides containing a C- or N-terminal
XX cysteine. These peptides are used in the method of the present invention
SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : ||| |
Db 3 FCISINITW 11

RESULT 38
ABU14171
ID ABU14171 standard; peptide; 12 AA.

XX AC ABU14171;

XX DT 28-FEB-2003 (first entry)

XX DE N-terminal bromoacetamide containing hFSH peptide #98.

XX KW Biomolecule detection; pixel array; micro-array support;
XX KW molecule binding; binding molecule; support surface; surface patch;
XX KW high density arraying; enzyme-linked-assay; bromoacetamide group;
XX KW human follicle-stimulating hormone; hFSH.

XX OS Homo sapiens.

XX PN WO200266984-A2.

XX PD 29-AUG-2002.

XX PF 15-FEB-2002; 2002WO-NL000097.

XX PR 16-FEB-2001; 2001EP-00200551.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Puijk WC, Van Dijk E, Slootstra JW;

XX DR WPI; 2003-103161/09.

XX PT Novel support used for micro-arrays and its use in detection of (bio)
XX PT molecules.

XX PS Example 3; Fig 6B; 4lpp; English.

XX CC The present invention relates to a method for the detection of
XX CC biomolecules in pixel arrays and the supports used for the micro-arrays.
XX CC The novel supports for the micro-arrays are suitable for determining the
XX CC binding of a first member molecule within a library of spots of tentative
XX CC first member binding molecules with a second member binding molecule. The
XX CC support is provided with a support surface where surface patches are
XX CC interspersed with surface areas that are materially distinct from the
XX CC patches. The support and method of the invention are useful for
XX CC identifying or obtaining a synthetic molecule comprising a binding site,
XX CC or a binding molecule capable of binding to a binding site. The molecule
XX CC is useful for interfering with, or effecting binding to a binding
XX CC molecule. The novel support for a micro-array and the method provide high
XX CC density arraying (testing many binding events in one go) and enzyme-
XX CC linked-assays (very sensitive) allowing the detection of more binding
XX CC pairs more rapidly. ABU14074-ABU14254 represent human follicle-
XX CC stimulating hormone (hFSH) derived peptides containing an N-terminal
XX CC bromoacetamide group. These peptides are used in the method of the
XX CC present invention

XX SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |
Db 3 FCISINTTW 11

RESULT 39

ABU14170
ID ABU14170 standard; peptide; 12 AA.

XX AC ABU14170;
XX DT 28-FEB-2003 (first entry)

XX DE N-terminal bromoacetamide containing hFSH peptide #97.

XX KW Biomolecule detection; pixel array; micro-array support;
XX KW molecule binding; binding molecule; support surface; surface patch;
XX KW high density arraying; enzyme-linked-assay; bromoacetamide group;
XX KW human follicle-stimulating hormone; hFSH.

XX OS Homo sapiens.

XX PN WO200266984-A2.

XX PD 29-AUG-2002.

XX PF 15-FEB-2002; 2002WO-NL000097.

XX PR 16-FEB-2001; 2001EP-00200551.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Puijk WC, Van Dijk E, Slootstra JW;

XX DR WPI; 2003-103161/09.

XX PT Novel support used for micro-arrays and its use in detection of (bio)

XX PT molecules.

XX PS Example 3; Fig 6B; 41pp; English.

CC The present invention relates to a method for the detection of

CC biomolecules in pixel arrays and the supports used for the micro-arrays.

CC The novel supports for the micro-arrays are suitable for determining the

CC binding of a first member molecule within a library of spots of tentative

CC first member binding molecules with a second member binding molecule. The

CC support is provided with a support surface where surface patches are

CC interspersed with surface areas that are materially distinct from the

CC patches. The support and method of the invention are useful for

CC identifying or obtaining a synthetic molecule comprising a binding site,

CC or a binding molecule capable of binding to a binding site. The molecule

CC is useful for interfering with, or effecting binding to a binding

CC molecule. The novel support for a micro-array and the method provide high

CC density arraying (testing many binding events in one go) and enzyme-

CC linked-assays (very sensitive) allowing the detection of more binding

CC pairs more rapidly. ABU14074-ABU14254 represent human follicle-

CC stimulating hormone (hFSH) derived peptides containing an N-terminal

CC bromoacetamide group. These peptides are used in the method of the

XX present invention

XX SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.1e+03;

Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |

Db 4 FCISINTTW 12

RESULT 40

ABU14355
ID ABU14355 standard; peptide; 12 AA.

XX AC ABU14355;
XX DT 12-MAR-2003 (first entry)

XX DE C- or N-terminal cysteine containing hFSH peptide #101.

XX KW Biomolecule detection; pixel array; micro-array support;
XX KW molecule binding; binding molecule; support surface; surface patch;
XX KW high density arraying; enzyme-linked-assay; hFSH;
XX KW human follicle-stimulating hormone.

XX OS Homo sapiens.

XX PN WO200266984-A2.

XX PD 29-AUG-2002.

XX PF 15-FEB-2002; 2002WO-NL000097.

XX PR 16-FEB-2001; 2001EP-00200551.

XX PA (PEPS-) PEPSCAN SYSTEMS BV.

XX PI Puijk WC, Van Dijk E, Slootstra JW;

XX DR WPI; 2003-103161/09.

XX PT Novel support used for micro-arrays and its use in detection of (bio)

XX PT molecules.

XX PS Example 3; Fig 6C; 41pp; English.

CC The present invention relates to a method for the detection of

CC biomolecules in pixel arrays and the supports used for the micro-arrays.

CC The novel supports for the micro-arrays are suitable for determining the

CC binding of a first member molecule within a library of spots of tentative

CC first member binding molecules with a second member binding molecule. The

CC support is provided with a support surface where surface patches are

CC interspersed with surface areas that are materially distinct from the

CC patches. The support and method of the invention are useful for

CC identifying or obtaining a synthetic molecule comprising a binding site,

CC or a binding molecule capable of binding to a binding site. The molecule

CC is useful for interfering with, or effecting binding to a binding

CC molecule. The novel support for a micro-array and the method provide high

CC density arraying (testing many binding events in one go) and enzyme-

CC linked-assays (very sensitive) allowing the detection of more binding

CC pairs more rapidly. ABU14255-ABU14437 represent human follicle-

CC stimulating hormone (hFSH) derived peptides containing a C- or N-terminal

CC cysteine. These peptides are used in the method of the present invention

XX SQ Sequence 12 AA;

RESULT 41

ABU14172
ID ABU14172 standard; peptide; 12 AA.

XX AC ABU14172;
XX DT 28-FEB-2003 (first entry)

```

XX DE N-terminal bromoacetamide containing hFSH peptide #99.
XX KW Biomolecule detection; pixel array; micro-array support;
KW KW molecule binding; binding molecule; support surface; surface patch;
KW KW high density arraying; enzyme-linked-assay; bromoacetamide group;
KW KW human follicle-stimulating hormone; hFSH.
XX OS Homo sapiens.
XX XX WO200266984-A2.
XX PN 29-AUG-2002.
XX PD 15-FEB-2002; 2002WO-NL000097.
XX PF 16-FEB-2001; 2001EP-00200551.
XX PR (PEPS-) PEPSCAN SYSTEMS BV.
XX PA Puijk WC, Van Dijk E, Slootstra JW;
XX PI WPI; 2003-103161/09.
XX DR Novel support used for micro-arrays and its use in detection of (bio)
XX PT molecules.
XX PT Example 3; Fig 6B; 41pp; English.
XX PS The present invention relates to a method for the detection of
XX CC biomolecules in pixel arrays and the supports used for the micro-arrays.
XX CC The novel supports for the micro-arrays are suitable for determining the
XX CC binding of a first member molecule within a library of spots of tentative
XX CC first member binding molecules with a second member binding molecule. The
XX CC support is provided with a support surface where surface patches are
XX CC interspersed with surface areas that are materially distinct from the
XX CC patches. The support and method of the invention are useful for
XX CC identifying or obtaining a synthetic molecule comprising a binding site,
XX CC or a binding molecule capable of binding to a binding site. The molecule
XX CC is useful for interfering with, or effecting binding to a binding
XX CC molecule. The novel support for a micro-array and the method provide high
XX CC density arraying (testing many binding events in one go) and enzyme-
XX CC linked-assays (very sensitive) allowing the detection of more binding
XX CC pairs more rapidly. ABU14074-ABU14254 represent human follicle-
XX CC stimulating hormone (hFSH) derived peptides containing an N-terminal
XX CC bromoacetamide group. These peptides are used in the method of the
XX CC present invention
XX SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |
Db 2 FCISINTTW 10

RESULT 42
ABU14353
ID ABU14353 standard; peptide; 12 AA.
XX AC ABU14353;
XX DT 12-MAR-2003 (first entry)
XX DE C- or N-terminal cysteine containing hFSH peptide #99.
XX KW Biomolecule detection; pixel array; micro-array support;
KW KW molecule binding; binding molecule; support surface; surface patch;
KW KW high density arraying; enzyme-linked-assay; hFSH;
KW KW human follicle-stimulating hormone.

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XX OS Homo sapiens.
XX PN WO200266984-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-NL000097.
XX PR 16-FEB-2001; 2001EP-00200551.
XX PA (PEPS-) PEPSCAN SYSTEMS BV.
XX PI Puijk WC, Van Dijk E, Slootstra JW;
XX DR WPI; 2003-103161/09.
XX PT Novel support used for micro-arrays and its use in detection of (bio)
XX PT molecules.
XX PS Example 3; Fig 6C; 41pp; English.
XX CC The present invention relates to a method for the detection of
XX CC biomolecules in pixel arrays and the supports used for the micro-arrays.
XX CC The novel supports for the micro-arrays are suitable for determining the
XX CC binding of a first member molecule within a library of spots of tentative
XX CC first member binding molecules with a second member binding molecule. The
XX CC support is provided with a support surface where surface patches are
XX CC interspersed with surface areas that are materially distinct from the
XX CC patches. The support and method of the invention are useful for
XX CC identifying or obtaining a synthetic molecule comprising a binding site,
XX CC or a binding molecule capable of binding to a binding site. The molecule
XX CC is useful for interfering with, or effecting binding to a binding
XX CC molecule. The novel support for a micro-array and the method provide high
XX CC density arraying (testing many binding events in one go) and enzyme-
XX CC linked-assays (very sensitive) allowing the detection of more binding
XX CC pairs more rapidly. ABU14255-ABU14437 represent human follicle-
XX CC stimulating hormone (hFSH) derived peptides containing a C- or N-terminal
XX CC cysteine. These peptides are used in the method of the present invention
XX SQ Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
| : : |
Db 3 FCISINTTW 11

RESULT 43
ABU14173
ID ABU14173 standard; peptide; 12 AA.
XX AC ABU14173;
XX DT 28-FEB-2003 (first entry)
XX DE N-terminal bromoacetamide containing hFSH peptide #100.
XX KW Biomolecule detection; pixel array; micro-array support;
KW KW molecule binding; binding molecule; support surface; surface patch;
KW KW high density arraying; enzyme-linked-assay; bromoacetamide group;
KW KW human follicle-stimulating hormone; hFSH.
XX OS Homo sapiens.
XX PN WO200266984-A2.
XX PD 29-AUG-2002.
XX PF 15-FEB-2002; 2002WO-NL000097.

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XX 16-FEB-2001; 2001EP-00200551.
XX (PEPS-) PEPS-SCAN SYSTEMS BV.
XX Puijk WC, Van Dijk E, Slootstra JW;
XX WPI; 2003-103161/09.
XX
XX Novel support used for micro-arrays and its use in detection of (bio)
XX molecules.
XX
XX Example 3; Fig 6B; 41pp; English.
XX
XX The present invention relates to a method for the detection of
XX biomolecules in pixel arrays and the supports used for the micro-arrays.
XX The novel supports for the micro-arrays are suitable for determining the
XX binding of a first member molecule within a library of spots of tentative
XX first member binding molecules with a second member binding molecule. The
XX support is provided with a support surface where surface patches are
XX interspersed with surface areas that are materially distinct from the
XX patches. The support and method of the invention are useful for
XX identifying or obtaining a synthetic molecule comprising a binding site,
XX or a binding molecule capable of binding to a binding site. The molecule
XX is useful for interfering with, or effecting binding to a binding
XX molecule. The novel support for a micro-array and the method provide high
XX density arrays (testing many binding events in one go) and enzyme-
XX linked-assays (very sensitive) allowing the detection of more binding
XX pairs more rapidly. ABU14074-ABU14254 represent human follicle-
XX stimulating hormone (hFSH) derived peptides containing an N-terminal
XX bromoacetamide group. These peptides are used in the method of the
XX present invention
XX
XX Sequence 12 AA;

Query Match 43.6%; Score 24; DB 6; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FTTVKTAW 10
| : : : |
Db 1 FCISINTW 9

RESULT 44
AAB38907
ID AAB38907 standard; peptide; 13 AA.

XX AAB38907;
XX
XX 02-FEB-2001 (first entry)
XX
XX HIV-1 peptide epitope #260.
XX
XX Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX
XX Human immunodeficiency virus.

XX WO200058438-A2.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-US008232.
XX
XX 29-MAR-1999; 99US-0126938P.

XX (BERN/) BERNSTEIN D.
XX (CHOW/) CHOWDHURY A.
XX (KOZH/) KOZHICH A.
XX (MOTS/) MOTSENBOCKER M.
XX
XX Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX

DR WPI; 2000-656164/63.
XX
XX Synthetic peptides useful for preventing and treating HIV infection in
XX mammals, comprising a conformationally constrained portion and a portion
XX with continuous stretch of amino acids of predicted secondary structure.
XX
XX Disclosure; Page 26; 69pp; English.
XX
XX The present invention relates to peptides (AAB38648-B38970) comprising a
XX first conformationally constrained portion with a cross-linked group of a
XX HIV envelope protein that induces neutralising antibodies, and a second
XX portion comprising a continuous stretch of at least 5 amino acids having
XX a predicted secondary structure. The present sequence is one such
XX peptide. The peptides of the present invention are useful as a vaccine
XX for prophylactic or therapeutic treatment of a mammal for HIV infection
XX
XX Sequence 13 AA;

Query Match 43.6%; Score 24; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 4 TTVK--TAW 10
| | | | |
Db 3 TTVKWNITW 11

RESULT 45
AAB38843
ID AAB38843 standard; peptide; 13 AA.

XX AAB38843;
XX
XX 02-FEB-2001 (first entry)
XX
XX HIV-1 peptide epitope #196.
XX
XX Vaccine; anti-HIV; HIV envelope protein; HIV infection.
XX
XX Human immunodeficiency virus.

XX WO200058438-A2.
XX
XX 05-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-US008232.
XX
XX 29-MAR-1999; 99US-0126938P.

XX (BERN/) BERNSTEIN D.
XX (CHOW/) CHOWDHURY A.
XX (KOZH/) KOZHICH A.
XX (MOTS/) MOTSENBOCKER M.
XX

XX Bernstein D, Chowdhury A, Kozhich A, Motsenbocker M;
XX
XX WPI; 2000-656164/63.

XX Synthetic peptides useful for preventing and treating HIV infection in
XX mammals, comprising a conformationally constrained portion and a portion
XX with continuous stretch of amino acids of predicted secondary structure.
XX
XX Disclosure; Page 24; 69pp; English.

XX The present invention relates to peptides (AAB38648-B38970) comprising a
XX first conformationally constrained portion with a cross-linked group of a
XX HIV envelope protein that induces neutralising antibodies, and a second
XX portion comprising a continuous stretch of at least 5 amino acids having
XX a predicted secondary structure. The present sequence is one such
XX peptide. The peptides of the present invention are useful as a vaccine
XX for prophylactic or therapeutic treatment of a mammal for HIV infection
XX
XX Sequence 13 AA;

Query Match 43.6%; Score 24; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 4 TTVK--TAW 10
| | | | |
Db 3 TTVKNNITW 11

Search completed: August 30, 2004, 10:49:40
Job time : 17.8986 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 9.62838 Seconds

(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-9

Perfect score: 55

Sequence: 1 FFTVKTAW 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	43.6	14	8 Q9TEN1	Q9ten1 anas castan
2	24	43.6	14	8 Q9TEN3	Q9ten3 anas gracil
3	23.5	42.7	14	8 Q8HGT1	Q8hgt1 gadus morhu
4	22	40.0	12	12 Q80IG7	Q80ig7 choristoneu
5	21	38.2	13	6 Q18890	Q18890 ateleas belz
6	20	36.4	8	2 Q9RE0	Q9re0 bacillus su
7	20	36.4	9	6 Q28093	Q28093 bos taurus
8	19	34.5	8	4 Q15902	Q15902 homo sapien
9	19	34.5	9	8 Q9T2K9	Q9t2k9 spinacia ol
10	18.5	33.6	13	11 Q9QW45	Q9qw45 rattus sp.
11	18	32.7	8	11 Q35835	Q35835 rattus sp.
12	18	32.7	9	2 P83529	P83529 lactobacill
13	18	32.7	11	2 Q9R446	Q9r446 neisseria g
14	18	32.7	12	4 Q16405	Q16405 homo sapien
15	18	32.7	13	10 Q42373	Q42373 solanum tub
16	18	32.7	14	4 Q8IVK4	Q8ivk4 homo sapien

17	17	30.9	9	4	Q99887	Q99887 homo sapien
18	17	30.9	11	8	Q9G356	Q9g356 agama atra
19	17	30.9	13	13	Q90XG9	Q90xg9 gallus gall
20	17	30.9	14	4	O75692	O75692 homo sapien
21	16	29.1	8	8	Q9T2W0	Q9t2w0 saccharomyc
22	16	29.1	9	2	Q9R635	Q9r635 chlamydia t
23	16	29.1	9	2	Q9R5M1	Q9r5m1 staphylococ
24	16	29.1	9	4	Q9H3Y3	Q9h3y3 homo sapien
25	16	29.1	9	4	Q15896	Q15896 homo sapien
26	16	29.1	10	6	Q9TRU6	Q9tr6 bos taurus
27	16	29.1	11	2	P83537	P83537 lactobacill
28	16	29.1	12	2	Q46039	Q46039 citrobacter
29	16	29.1	12	10	Q9M433	Q9m433 lotus japon
30	16	29.1	12	10	Q8GSB9	Q8gsb9 lolium pere
31	16	29.1	12	11	Q64242	Q64242 rattus sp.
32	16	29.1	13	2	Q9ZE21	Q9ze21 buchnera ap
33	15	27.3	8	8	Q94VC1	Q94vc1 varanus rud
34	15	27.3	8	8	Q94VF6	Q94vf6 varanus job
35	15	27.3	8	8	Q94V88	Q94v88 varanus tri
36	15	27.3	8	8	Q94V91	Q94v91 varanus tim
37	15	27.3	8	8	Q94VE4	Q94ve4 varanus mel
38	15	27.3	8	8	Q94VB2	Q94vb2 varanus sal
39	15	27.3	8	8	Q94VF9	Q94vf9 varanus ind
40	15	27.3	8	8	Q94VA7	Q94va7 varanus sal
41	15	27.3	8	8	Q94VB5	Q94vb5 varanus sal
42	15	27.3	8	11	P70243	P70243 mus musculu
43	15	27.3	9	4	Q9H326	Q9h326 homo sapien
44	15	27.3	9	8	Q9T688	Q9t688 gecko gecko
45	15	27.3	9	8	Q94VD8	Q94vd8 varanus nil

ALIGNMENTS

RESULT 1

Q9TEN1	ID	Q9TEN1	PRELIMINARY;	PRT;	14 AA.
AC	Q9TEN1;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE	ATPase 8 (Fragment)				
OS	Anas castanea (Chestnut teal).				
OG	Mitochondrion.				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauia; Aves; Neognathae; Anseriformes; Anatidae; Anas.				
OX	NCBI_TaxID=45631;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kennedy M., Spencer H.G.;				
RT	"Phylogeny, Biogeography, and Taxonomy of Australasian Teals."				
RL	Auk 0:0-0(2000).				
DR	EMBL; AF173494; AAD51052.1; -.				
DR	GO; GO:0005739; C:mitochondrion; IEA.				
KW	Mitochondrion.				
FT	NON TER				
SQ	SEQUENCE 14 AA; 1672 MW; 80FB803727F9B871 CRC64;				

Query Match 43.6%; Score 24; DB 8; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 ITTVKTAW 10
: ||| |
Db 2 LTTKPTPW 9

RESULT 2

Q9TEN3	ID	Q9TEN3	PRELIMINARY;	PRT;	14 AA.
AC	Q9TEN3;				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE ATPase 8 (Fragment).
 OS Anas gracilis (Grey teal).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=45630;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kennedy M., Spencer H.G.;
 RT "Phylogeny, Biogeography, and Taxonomy of Australasian Teals.";
 RL Auk 0:0-0(2000).
 DR EMBL; AF173493; AAD51050.1; --
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1572 MW; 80FB803727F9B871 CRC64;
 Query Match 43.6%; Score 24; DB 8; Length 14;
 Best Local Similarity 50.0%; Pred. No. 7.9e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 ITTVKTAW 10
 Db :||| |
 2 LTTKTPW 9
 RESULT 3
 Q8HG7L PRELIMINARY; PRT; 14 AA.
 ID Q8HG7L
 AC Q8HG7L
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE ATPase 8 (Fragment)
 OS Gadus morhua (Atlantic cod).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Taylor M.I., Fox C., Rico I., Rico C.;
 RT "Species-specific TagMan probes for simultaneous identification of
 (Gadus morhua L.), haddock (Melanogrammus aeglefinus L.) and whiting
 (Merlangius merlangus L.)";
 RT Mol. Ecol. Notes 2:599-601(2002).
 DR EMBL; AF526615; AAN85062.1; --
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1753 MW; D4AF852330085E6D CRC64;
 Query Match 42.7%; Score 23.5; DB 8; Length 14;
 Best Local Similarity 66.7%; Pred. No. 9.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 3 ITTVKTA-W 10
 Db :||| |
 1 MTTPKTAPW 9
 RESULT 4
 Q80IG7 PRELIMINARY; PRT; 12 AA.
 ID Q80IG7
 AC Q80IG7
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Mini-cistron protein.
 OS Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV).

OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=208973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carstens E.B.;
 RT "Identification and analysis of the CfMNPV p143 gene.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF127530; AAF36457.1; --
 SQ SEQUENCE 12 AA; 1252 MW; C878D87A88B2CDD9 CRC64;
 Query Match 40.0%; Score 22; DB 12; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 FFITTVKVT 8
 Db :||| |
 5 FAVTTPRT 12
 RESULT 5
 O18890 PRELIMINARY; PRT; 13 AA.
 ID O18890
 AC O18890
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Granzyme B (Fragment).
 OS Ateles belzebuth chamek (Chamek spider monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
 OX NCBI_TaxID=118643;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98267189; PubMed=9601975;
 RA Canavez F., Moreira M.A.M., Bonvicino C.R., Parham P., Seunarez H.N.;
 RT "Comparative gene assignment in Ateles paniscus chamek (Platyrrhini,
 Primates) and man: association of three separate human syntenic groups
 and evolutionary considerations.";
 RL Chromosoma 107:73-79(1998).
 DR EMBL; AF029165; AAB84196.1; --
 DR GO; GO:0004295; P:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001254; Peptidase S1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1394 MW; C0FF86B8F4E5EDDD CRC64;
 Query Match 38.2%; Score 21; DB 6; Length 13;
 Best Local Similarity 33.3%; Pred. No. 2.9e+03;
 Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 FITTVKTAW 10
 Db :||| |
 2 FVLTAACHW 10
 RESULT 6
 Q9R9E0 PRELIMINARY; PRT; 8 AA.
 ID Q9R9E0
 AC Q9R9E0
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
 DE Stage V sporulation protein E (Fragment).
 GN SPOVE.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;


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RX MEDLINE=93003529; PubMed=1391053;
RA Henriques A.O., de Lencastre H., Piggot P.J.;
RT "A Bacillus subtilis morphogene cluster that includes spore is
RT homologous to the mra region of Escherichia coli.";
RL Biochimie 74:735-748(1992).
DR EMBL; X64258; CAA45556.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 893 MW; E575A1A33321B1A6 CRC64;

Query Match 36.4%; Score 20; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKTA 9
Db :|||:
1 MTTKTS 7

RESULT 7
Q28093 ID Q28093 PRELIMINARY; PRT; 9 AA.
AC Q28093;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytokeratin IV gene upstream region (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89231609; PubMed=2469572;
RA Blessing M., Jorcano J.L., Franke W.W.;
RT "Enhancer elements directing cell-type-specific expression of
RT cytokeratin genes and changes of the epithelial cytoskeleton by
RT transfections of hybrid cytokeratin genes.";
RL EMBO J. 8:117-126(1989).
DR EMBL; X14478; CAA32640.1; -.
DR PIR; I46016; I46016.
DR GO; GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1044 MW; 819A22D1B5B32B45 CRC64;

Query Match 36.4%; Score 20; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTVKKT 8
Db :|||:
5 STVKT 9

RESULT 8
Q15902 ID Q15902 PRELIMINARY; PRT; 8 AA.
AC Q15902;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP7E7A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUP=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;

RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32081; AAA73892.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 931 MW; 83D699CAB1B1B2C9 CRC64;

Query Match 34.5%; Score 19; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITT 5
Db :|||:
1 FVTT 4

RESULT 9
Q9T2K9 ID Q9T2K9 PRELIMINARY; PRT; 9 AA.
AC Q9T2K9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LHC II=LIGHT-harvesting chlorophyll protein II (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=91373386; PubMed=1894641;
RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.;
RT "Tandem mass spectrometry identifies sites of three post-translational
RT modifications of spinach light-harvesting chlorophyll protein II.
RT Proteolytic cleavage, acetylation, and phosphorylation.";
RL J. Biol. Chem. 266:17584-17591(1991).
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1042 MW; 6B5D6DC5B322D1B4 CRC64;

Query Match 34.5%; Score 19; DB 8; Length 9;
Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TVKTA 9
Db :|||:
3 TVKSA 7

RESULT 10
Q9QW45 ID Q9QW45 PRELIMINARY; PRT; 13 AA.
AC Q9QW45;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GTP-binding protein RAB16 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054572; PubMed=1429617;
RA Eiferink L.A., Anzai K., Scheller R.H.;
RT "Rab15, a novel low molecular weight GTP-binding protein specifically
RT expressed in rat brain.";
RL J. Biol. Chem. 267:22693-22693(1992).
FT NON_TER 1 1
FT NON_TER 13 13

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SQ SEQUENCE 13 AA; 1584 MW; 40B5FE7236041A3 CRC64;

Query Match      33.6%; Score 18.5; DB 11; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.9e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 4 ITVKT-AW 10
   |::|
Db 3 TQIKTYSW 10

RESULT 11
Q35835
ID O35835 PRELIMINARY; PRT; 8 AA.
AC O35835;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ORF1 protein.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
RT NR0 convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779 (1997).
DR EMBL; X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA; 886 MW; EA7EALB1ADC5A5B6 CRC64;

Query Match      32.7%; Score 18; DB 11; Length 8;
Best Local Similarity 25.0%; Pred. No. 1e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 ITVKTAW 10
   |::|
Db 1 MSSATCW 8

RESULT 12
P83529
ID P83529 PRELIMINARY; PRT; 9 AA.
AC P83529;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA "Draws O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774 (2002).
CC -!- MISCELLANEOUS; ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
CC PROTEIN IS: 15 KDA.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 988 MW; 1031B1B1A729C86B CRC64;

Query Match      32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 FITT 5
   |::|
Db 4 FITT 7

RESULT 13
Q9R446
ID Q9R446 PRELIMINARY; PRT; 11 AA.
AC Q9R446;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Carbamoyl-phosphate synthase subunit A (Fragment).
CARA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billows F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MS11, and FA1090;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF029363; AAC78453.1; -.
DR EMBL; AF029362; AAC78452.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DD33694 CRC64;

Query Match      32.7%; Score 18; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FITTVKTA 9
   |::|
Db 1 FIGNKKAA 8

RESULT 14
Q16405
ID Q16405 PRELIMINARY; PRT; 12 AA.
AC Q16405;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Estrogen receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92140401; PubMed=1779972;
RA Wang Y., Miksicek R.J.;
RT "Identification of a dominant negative form of the human estrogen
RT receptor.";
RL Mol. Endocrinol. 5:1707-1715 (1991).
DR EMBL; S79911; AAB21301.1; -.
DR PIR; I77529; I77529.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1280 MW; 5A876633B3A37DD3 CRC64;
```

Query Match 32.7%; Score 18; DB 4; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
 : : : :
 Db 2 SVTKAW 7

RESULT 15

Q42373 ID Q42373 PRELIMINARY; PRT; 13 AA.
 AC Q42373;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Patatin class I (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88226014; PubMed=3371664;
 RA Mignery G.A., Pikaard C.S., Park W.D.;
 RT "Molecular characterization of the patatin multigene family of
 potato.";
 RL Gene 62:27-44(1988).
 DR EMBL; M18882; AAA33829.1; -;
 DR EMBL; M18881; AAA33829.1; -;
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1456 MW; 916595F37A6E29D5 CRC64;

Query Match 32.7%; Score 18; DB 10; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTV 6
 : : : :
 Db 7 FLIITV 12

RESULT 16

Q81VK4 ID Q81VK4 PRELIMINARY; PRT; 14 AA.
 AC Q81VK4;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Steerin2 protein (Fragment).
 GN STEERIN2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,
 RA Geysen J.J.G.H.;
 RT "Sensorineural defects in mice hypomorphic for a mammalian homolog of
 unc-53.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ488207; CAD32560.1; -;
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1267 MW; C67BE72BA83F9CED CRC64;

Query Match 32.7%; Score 18; DB 4; Length 14;
 Best Local Similarity 28.6%; Pred. No. 1.2e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTVKTAW 10

Db 4 TSAASSW 10

RESULT 17

Q99887 ID Q99887 PRELIMINARY; PRT; 9 AA.
 AC Q99887;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE 11 <beta>-HSD2 protein (Fragment).
 GN 11 <beta>-HSD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96133030; PubMed=8538347;
 RA Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howie A.J.,
 RA Sheppard M.C., Whorwood C.B.;
 RT "Hypertension in the syndrome of apparent mineralocorticoid excess due
 to mutation of the 11 beta-hydroxysteroid dehydrogenase type 2 gene.";
 RL Lancet 347:88-91(1996).
 DR EMBL; S80133; AAD14324.1; -;
 DR GO; GO:0003845; F:11-beta-hydroxysteroid dehydrogenase activity; NAS.
 DR GO; GO:0008212; P:mineralocorticoid metabolism; NAS.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1020 MW; CEF2EB1F5B059C9 CRC64;

Query Match 30.9%; Score 17; DB 4; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFIT 4
 : : : :
 Db 2 FFIS 5

RESULT 18

Q9G356 ID Q9G356 PRELIMINARY; PRT; 11 AA.
 AC Q9G356;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Agama atra (Southern rock agama).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.
 OX NCBI_TaxID=52208;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;

RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics."
RL Syst. Biol. 49:233-256 (2000).
DR EMBL; AF128505; AAG00752.1; --
GO GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1402 MW; B052EC10D36411A6 CRC64;

Query Match 30.9%; Score 17; DB 8; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
DB 2 TVKTAW 7

RESULT 19
Q90XG9 PRELIMINARY; PRT; 13 AA.
AC Q90XG9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pdc4 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363043; PubMed=11470166;
RA Schlichter U., Kattmann D., Appl H., Miethe J., Brehmer-Fastnacht A.,
RA Klemmner K.-H.;
RT "Identification of the myb-inducible promoter of the chicken Pdc4
gene."
RL Biochim. Biophys. Acta 1520:99-104 (2001).
DR EMBL; AF382032; AAK59968.1; --
FT NON TER 13
SQ SEQUENCE 13 AA; 1577 MW; DF23PEC8057EC1F6 CRC64;

Query Match 30.9%; Score 17; DB 13; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITTV 6
DB 9 YISTV 13

RESULT 20
O75692 PRELIMINARY; PRT; 14 AA.
AC O75692;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN GTT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Visvikis A.;
RT "Identification of promoter sequences driving the expression of type
III human gamma-glutamyltransferase mRNAs."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ006789; CAA07253.1; --
KW Hypothetical protein.

FT NON TER 14
SQ SEQUENCE 14 AA; 1641 MW; D8CE5693986DE4C2 CRC64;
Query Match 30.9%; Score 17; DB 4; Length 14;
Best Local Similarity 28.6%; Pred. No. 1.9e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 FEITTVK 7
DB 5 FFVAQLR 11

RESULT 21
Q9T2W0 PRELIMINARY; PRT; 8 AA.
AC Q9T2W0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE CBI1 PRECURSOR=PROTEOLYTIC processing site (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=92035078; PubMed=1657414;
RA Korte A., Michaelis U., Lottspeich F., Rodel G.;
RT "Over-expression, purification and determination of the proteolytic
processing site of the yeast mitochondrial CBI1 protein."
RL Curr. Genet. 20:87-90 (1991).
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 913 MW; 72D1A44041B40047 CRC64;

Query Match 29.1%; Score 16; DB 8; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKT 8
DB 2 IRTINT 7

RESULT 22
Q9RG35 PRELIMINARY; PRT; 9 AA.
AC Q9RG35;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Major outer membrane protein variable domain IV, MOMP VD IV
(Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92040090; PubMed=1718870;
RA Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;
RT "Functional and structural mapping of Chlamydia trachomatis species-
specific major outer membrane protein epitopes by use of neutralizing
monoclonal antibodies."
RL Infect. Immun. 59:4147-4153 (1991).
DR FIR; S16034; S16034.
FT NON TER 1
FT NON TER 9
SQ SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      8 TAW 10
Db      1 TTW 3

RESULT 23
Q9R5M1 PRELIMINARY; PRT; 9 AA.
ID Q9R5M1
AC Q9R5M1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE
RX MEDLINE=92176005; PubMed=1541563;
RA Liang O.D., Ascencio F., Fransson L.A., Wadstrom T.;
RT "Binding of heparan sulfate to Staphylococcus aureus.";
RL Infect. Immun. 60:899-906(1992).
DR PIR; A43848; A43848.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 990 MW; 2289DDDD7337861B3 CRC64;

Query Match 29.1%; Score 16; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY      8 TAW 10
Db      3 TGV 5

RESULT 24
Q9H3Y3 PRELIMINARY; PRT; 9 AA.
ID Q9H3Y3
AC Q9H3Y3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE D9839B11.1 (Novel protein with a kunitz/bovine pancreatic trypsin
inhibitor domain and WAP-type (Whey acidic protein) 'four-disulfide
core' domains) (Fragment).
GN D9461P17.1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121778; CAB76844.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 TVKT 8
Db      3 TVRT 6

RESULT 25
Q15896 PRELIMINARY; PRT; 9 AA.
ID Q15896
AC Q15896;

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP6A10B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32076; AAA73886.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; 11D15731B2C9C054 CRC64;

Query Match 29.1%; Score 16; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 FITTV 6
Db      4 FVTLL 8

RESULT 26
Q9TRU6 PRELIMINARY; PRT; 10 AA.
ID Q9TRU6
AC Q9TRU6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GAP-3, GTPase-activating protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92112869; PubMed=1309786;
RA Nice B.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
RA Burgess A.W.;
RT "The purification of a Rap1 GTPase-activating protein from bovine
RT brain cytosol.";
RL J. Biol. Chem. 267:1546-1553(1992).
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 29.1%; Score 16; DB 6; Length 10;
Best Local Similarity 33.3%; Pred. No. 2.1e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 FFITVTKTA 9
Db      1 FLITKLINA 9

RESULT 27
P83537 PRELIMINARY; PRT; 11 AA.
ID P83537
AC P83537;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).

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OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RX STRAIN=DSM 20451;
 RC PubMed=12112860;
 RA Dimou M., Roussis A., Katinakis P.;
 RT "High pressure effects step-wise altered protein expression in
 RT Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC -!- INDUCTION: BY ELAVATED HYDROSTATIC PRESSURE.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
 CC PROTEIN IS: 65 KDA.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;
 Query Match 29.1%; Score 16; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 2.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PFIT 4
 Db 3 PFAT 6
 RESULT 28
 Q46039 PRELIMINARY; PRT; 12 AA.
 ID Q46039
 AC Q46039;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE FRDB protein (fragment).
 GN FRDB.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89291719; PubMed=2786868;
 RA Lindquist S., Lindberg F., Normark S.;
 RT "Binding of the Citrobacter freundii AmpR regulator to a single DNA
 RT site provides both autoregulation and activation of the inducible ampC
 RT beta-lactamase gene.";
 RL J. Bacteriol. 171:3746-3753(1989).
 DR EMBL; M27222; AAA64511.1; -.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1214 MW; 968D697A24705DC1 CRC64;
 Query Match 29.1%; Score 16; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.5e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 TVKTA 9
 Db 2 TVVTA 6
 RESULT 29
 Q9M433 PRELIMINARY; PRT; 12 AA.
 ID Q9M433
 AC Q9M433;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE ENOD40-1 protein.
 GN ENOD40-1.
 OS Lotus japonicus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae; Lotus.
 OX NCBI_TaxID=34305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20427395; PubMed=10975655;
 RA Fletetakis E., Kavroulakis N., Quaedvlieg N.E.M., Spaink H.P.,
 RA Dimou M., Roussis A., Katinakis P.;
 RT "Lotus japonicus contains two distinct ENOD40 genes that are expressed
 RT in symbiotic, non-symbiotic and embryonic tissues.";
 RL Mol. Plant Microbe Interact. 13:987-994(2000).
 DR EMBL; AJ271787; CAB92978.1; -.
 SQ SEQUENCE 12 AA; 1403 MW; 3C6955187CB046C3 CRC64;
 Query Match 29.1%; Score 16; DB 10; Length 12;
 Best Local Similarity 40.0%; Pred. No. 2.5e+04;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 6 VKTAW 10
 Db 1 MKLCW 5
 RESULT 30
 Q8GSB9 PRELIMINARY; PRT; 12 AA.
 ID Q8GSB9
 AC Q8GSB9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ENOD40-like protein.
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Poaceae; Lolium.
 OX NCBI_TaxID=4522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Borvi; TISSUE=Stem;
 RA Larsen K.;
 RT "ENOD40 homolog from perennial ryegrass (Lolium perenne)." ;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Larsen K.;
 RT "ENOD40 gene from perennial ryegrass (Lolium perenne)." ;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF538350; AAN15133.1; -.
 DR EMBL; AF538351; AAN15134.1; -.
 SQ SEQUENCE 12 AA; 1455 MW; 3EF4B0A918EB1733 CRC64;
 Query Match 29.1%; Score 16; DB 10; Length 12;
 Best Local Similarity 40.0%; Pred. No. 2.5e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 VKTAW 10
 Db 1 MEDAW 5
 RESULT 31
 Q64242 PRELIMINARY; PRT; 12 AA.
 ID Q64242
 AC Q64242;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Sodium channel IIIa (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;

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RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92211397; PubMed=13133493;
RA  Schaller K.L., Krzemien D.M., McKenna N.M., Caldwell J.H.;
RT  "Alternatively spliced sodium channel transcripts in brain and
RL  muscle.";
RJ  J. Neurosci. 12:1370-1381(1992).
DR  EMBL; S97387; AAB21983.2; -.
DR  PIR; A44824; A44824.
FT  NON_TER 1
FT  NON_TER 12
SQ  SEQUENCE 12 AA; 1238 MW; 9C79B13247A866C5 CRC64;

Query Match      29.1%; Score 16; DB 11; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  4 TTVK 8
DB  |||
    8 TTET 12

RESULT 32
Q9ZEZ1
ID  Q9ZEZ1 PRELIMINARY; PRT; 13 AA.
AC  Q9ZEZ1;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DT  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN  LEUA
OS  Buchnera aphidicola.
OG  Plasmid pBPP1.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC  Enterobacteriaceae; Buchnera.
OX  NCBI_TaxID=9;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99028904; PubMed=9812361;
RA  Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT  "Structure and evolution of the leucine plasmids carried by the
RT  endosymbiont (Buchnera aphidicola) from aphids of the family
RT  Aphididae.";
RL  FEMS Microbiol. Lett. 168:43-49(1998).
DR  EMBL; AJ006877; CAA07302.1; -.
DR  GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR  GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR  GO; GO:0016829; F:lyase activity; IEA.
KW  Lyase; Plasmid.
FT  NON_TER 13
FT  NON_TER 13
SQ  SEQUENCE 13 AA; 1538 MW; 1BD1D0320390C050 CRC64;

Query Match      29.1%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  2 FITVK 7
DB  |||
    8 FDTLR 13

RESULT 33
Q94VCI
ID  Q94VCI PRELIMINARY; PRT; 8 AA.
AC  Q94VCI;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Cytochrome c oxidase subunit I (Fragment).
GN  COI.
OS  Varanus rudicollis (Rough-necked monitor).
OG  Mitochondrion.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC  Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX  NCBI_TaxID=169851;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Ast J.C.;
RT  "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL  Cladistics 17:0-0(2001).
DR  EMBL; AF407521; AAL10116.1; -.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON_TER 8
FT  NON_TER 8
SQ  SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

Query Match      27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  8 TAW 10
DB  |||
    2 TRW 4

RESULT 34
Q94VF6
ID  Q94VF6 PRELIMINARY; PRT; 8 AA.
AC  Q94VF6;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Cytochrome c oxidase subunit I (Fragment).
GN  COI.
OS  Varanus jobiensis (Peach throat monitor).
OG  Mitochondrion.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX  NCBI_TaxID=169843;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Ast J.C.;
RT  "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL  Cladistics 17:0-0(2001).
DR  EMBL; AF407507; AAL10075.1; -.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON_TER 8
FT  NON_TER 8
SQ  SEQUENCE 8 AA; 1144 MW; EFD729DB436411A6 CRC64;

Query Match      27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  8 TAW 10
DB  |||
    2 TRW 4

RESULT 35
Q94V88
ID  Q94V88 PRELIMINARY; PRT; 8 AA.
AC  Q94V88;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  Cytochrome c oxidase subunit I (Fragment).
GN  COI.
OS  Varanus tristis.
OG  Mitochondrion.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX  NCBI_TaxID=62052;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Ast J.C.;

```

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407533; AAL10151.1; --
KW GO; GO:0005739; C:mitochondrion; IEA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db |
2 TRW 4

RESULT 36
Q94V91 ID Q94V91 PRELIMINARY; PRT; 8 AA.
AC Q94V91;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus timorensis (Timor monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62053;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407532; AAL10148.1; --
KW GO; GO:0005739; C:mitochondrion; IEA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db |
2 TRW 4

RESULT 37
Q94VE4 ID Q94VE4 PRELIMINARY; PRT; 8 AA.
AC Q94VE4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus melinus (Quince monitor lizard).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169846;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407511; AAL10087.1; --
KW GO; GO:0005739; C:mitochondrion; IEA.

FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;
Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db |
2 TRW 4

RESULT 38
Q94VB2 ID Q94VB2 PRELIMINARY; PRT; 8 AA.
AC Q94VB2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus salvator togianus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169832;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407524; AAL10125.1; --
KW GO; GO:0005739; C:mitochondrion; IEA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db |
2 TRW 4

RESULT 39
Q94VF9 ID Q94VF9 PRELIMINARY; PRT; 8 AA.
AC Q94VF9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus indicus (Mangrove monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62043;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407506; AAL10072.1; --
KW GO; GO:0005739; C:mitochondrion; IEA.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1041 MW; E8B5B9C7336411A6 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10

Db 2 TRW 4

RESULT 40

Q94VA7 ID Q94VA7 PRELIMINARY; PRT; 8 AA.

AC Q94VA7; (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN COI.

OS Varanus salvator salvator.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=169831;

[1]

RN SEQUENCE FROM N.A.

RP Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

RL Cladistics 17:0-0(2001).

DR EMBL; AF407526; AAL10130.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 8

SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match

Best Local Similarity 27.3%; Score 15; DB 8; Length 8;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10

Db 2 TRW 4

RESULT 41

Q94VB5 ID Q94VB5 PRELIMINARY; PRT; 8 AA.

AC Q94VB5; (T-EMBLrel. 19, Created)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN COI.

OS Varanus salvator cumingi.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=169830;

[1]

RN SEQUENCE FROM N.A.

RP Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

RL Cladistics 17:0-0(2001).

DR EMBL; AF407523; AAL10122.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 8

SQ SEQUENCE 8 AA; 992 MW; EFC775A5A36411A6 CRC64;

Query Match

Best Local Similarity 27.3%; Score 15; DB 8; Length 8;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10

Db 2 TRW 4

RESULT 42

P70243 ID P70243 PRELIMINARY; PRT; 8 AA.

AC P70243; (T-EMBLrel. 02, Created)

DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)

DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DE Skeletal muscle-specific calcium channel (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=129;

RA Ophoff R.A.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; X98325; CAA66969.1; -.

FT NON TER 1

FT NON TER 8

SQ SEQUENCE 8 AA; 865 MW; D9C37DDB1861ADDE CRC64;

Query Match 27.3%; Score 15; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10

Db 6 AW 7

RESULT 43

Q9H326 ID Q9H326 PRELIMINARY; PRT; 9 AA.

AC Q9H326; (T-EMBLrel. 16, Created)

DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (T-EMBLrel. 16, Last annotation update)

DE NAD+-dependent isocitrate dehydrogenase 3 alpha subunit

(Fragment).

GN IDH3A.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Huh T.-L.;

RT "Structural and functional characterization of the human NAD+-

dependent isocitrate dehydrogenase alpha subunit promoter.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF157515; AAG43379.1; -.

FT NON TER 9

FT NON TER 9

SQ SEQUENCE 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match

Best Local Similarity 27.3%; Score 15; DB 4; Length 9;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10

Db 5 AW 6

RESULT 44

Q9T688 ID Q9T688 PRELIMINARY; PRT; 9 AA.

AC Q9T688; (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

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DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Gecko gecko (Tokay gecko).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Gekkota; Gekkonidae; Gekko.
OX NCBI_TaxID=36310;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343618; PubMed=10413626;
RA Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
RT "Vicariant patterns of fragmentation among gekkonid lizards of the
RT genus teratoscincus produced by the Indian collision: A molecular
RT phylogenetic perspective and an area cladogram for central asia.";
RL Mol. Phylogenet. Evol. 12:320-332(1999).
DR EMBL; AF114249; AAD51600.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 9 AA; 1188 MW; 428CB9CD36411A7 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFT 4
Db 6 FFT 9

RESULT 45
Q94VD8
ID Q94VD8 PRELIMINARY; PRT; 9 AA.
AC Q94VD8;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus niloticus (Nile monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407514; AAL10096.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 27.3%; Score 15; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
Db 4 TRW 6

Search completed: August 30, 2004, 10:55:30
Job time : 13.6284 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.72297 Seconds

(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-9

Perfect score: 55

Sequence: 1 FFITTVKTAW 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	30.9	9	1	PTSP_BOMMO
2	17	30.9	10	1	LABA_JATMU
3	16	29.1	8	1	AKHG_GRYBI
4	16	29.1	10	1	CA12_LITCI
5	16	29.1	10	1	CAER_LITXA
6	16	29.1	10	1	HTF_HELZE
7	16	29.1	11	1	CA31_LITCI
8	16	29.1	11	1	CA32_LITCI
9	16	29.1	12	1	CXAL_CONIM
10	16	29.1	12	1	NO40_SESRO
11	16	29.1	12	1	NO40_SOVEN
12	16	29.1	12	1	UH03_RAT
13	16	29.1	12	1	V25K_WSSV
14	16	29.1	14	1	NEJ2_FASHE
15	15	27.3	8	1	RT34_BOVIN
16	15	27.3	9	1	LMIP_LOCM
17	15	27.3	10	1	TKNK_FIG
18	15	27.3	10	1	TPIS_NICPL
19	15	27.3	12	1	YZFY_ECOLI
20	15	27.3	13	1	E121_LITRU
21	15	27.3	13	1	E122_LITRU
22	15	27.3	13	1	UHA3_CANFA
23	15	27.3	14	1	ALYT_ALYOB
24	15	27.3	14	1	LPF2_ECOLI
25	15	27.3	14	1	UC04_MAIZE
26	14	25.5	8	1	PLP_BRANA
27	14	25.5	12	1	PORD_METTM
28	14	25.5	13	1	YFNP_PHOLI
29	14	25.5	14	1	CXIA_CONBE
30	14	25.5	14	1	LPW_CITFR
31	14	25.5	14	1	LPW_ECOLI
32	13	23.6	8	1	AXH_TABAT
33	13	23.6	8	1	LCK5_LEUMA

34	13	23.6	8	1	LCK5_LEUMA
35	13	23.6	8	1	LCK7_LEUMA
36	13	23.6	10	1	AFE_CAPGI
37	13	23.6	10	1	COXQ_SHEEP
38	13	23.6	10	1	HTF_TABAT
39	13	23.6	12	1	UR2_POLSP
40	13	23.6	13	1	LIGB_TRAVE
41	13	23.6	13	1	TY13_PHYRO
42	13	23.6	14	1	KARA_BROPL
43	13	23.6	14	1	MCRX_METTM
44	13	23.6	14	1	SMS1_MYOSC
45	13	23.6	14	1	SMS_ALLMI

ALIGNMENTS

RESULT 1
PTSP_BOMMO
ID PTSP_BOMMO STANDARD; PRT; 9 AA.
AC P82003;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prothoracicostatic peptide (Bom-PTSP).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RC STRAIN=C145 X N140; TISSUE=Brain;
RX MEDLINE=20002634; PubMed=10531308;
RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA Kataoka H.;
RT "Identification of a prothoracicostatic peptide in the larval brain of
the silkworm, Bombyx mori";
RL J. Biol. Chem. 274:31169-31173 (1999).
RN [2]
RP ERRATUM.
RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA Kataoka H.;
RL J. Biol. Chem. 275:9892-9892(2000).
CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
gland.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: Early fifth instar.
KW Hormone; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1090 MW; 3878C5B4472AB6C3 CRC64;
AMIDATION.
Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 6 VKTAW 10
: : :
Db 5 LNSAW 9

RESULT 2
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Labaditin.
OS Jatropa multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaeae;

OC Jatropa.
OX NCBI_TaxID=3996;
RN [1]_ |
RC SEQUENCE.
RC TISSUE=Latex;
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropa
RT multifida L. (Euphorbiaceae). Isolation and sequence determination
RT by means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the
CC classical pathway of complement activation in vitro. Activity
CC seems to be based on an interaction with C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
CC for treatment of infected wounds, skin infections and scabies.
CC SEQUENCE 10 AA; 1089 MW; D98AAD6362DB18362 CRC64;
SQ
Query Match 30.9%; Score 17; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 VKTAW 10
DB 3 VMTVW 7
RESULT 3
AKHG GRVBI STANDARD; PRT; 8 AA.
ID AKHG GRVBI
AC P14086;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone G (AKH-G) (RO II).
OS Gryllus bimaculatus (two-spotted cricket), and
OS Romalea microptera (lubber grasshopper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllinae;
OC Gryllus.
OX NCBI_TaxID=6999, 7007;
RN [1]_ |
RC SEQUENCE.
RC SPECIES=G.bimaculatus; TISSUE=Corpora cardiaca;
RX MEDLINE=88106553; PubMed=3426616;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary sequence analysis by fast atom bombardment mass spectrometry
RT of a peptide with adipokinetic activity from the corpora cardiaca of
RT the cricket Gryllus bimaculatus.";
RL Biochem. Biophys. Res. Commun. 149:908-914(1987).
RN [2]
RP SEQUENCE.
RC SPECIES-R.microptera; TISSUE=Corpora cardiaca;
RX MEDLINE=89145002; PubMed=3226948;
RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT the lubber grasshopper, Romalea microptera.";
RL Peptides 9:681-688(1988).
CC -!- FUNCTION: This hormone, released from cells in the corpora
CC cardiaca after the beginning of flight, causes release of
CC diglycerides from the fat body and then stimulates the flight
CC muscles to use these diglycerides as an energy source.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / RPCH family.
CC PIR: A28004; A28004.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 938 MW; 867861B5B9C452D6 CRC64;
Query Match 29.1%; Score 16; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 TAW 10
DB 6 TGM 8
RESULT 4
CA12_LITCI STANDARD; PRT; 10 AA.
ID CA12_LITCI
AC P82086;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 1.2/1.2Y4.
OS Litoria citropa (Australian blue mountains tree frog), and
OS Litoria citropa (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770, 30345;
RN [1]_ |
RC SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).
RC SPECIES=L.citropa; TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC SPECIES=L.splendida; TISSUE=Skin secretion;
RX MEDLINE=20069371; PubMed=16601876;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT "Differences in the skin peptides of the male and female Australian
RT tree frog Litoria splendida. The discovery of the aquatic male sex
RT pheromone splendorpherin, together with Phe8 caerulein and the
RT antibiotic peptide caerin 1.10.";
RL Eur. J. Biochem. 267:269-275(2000).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 4 4 SULFATION.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;
Query Match 29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 TAW 10
DB 5 TGM 7
RESULT 5
CAER_LITXA STANDARD; PRT; 10 AA.
ID CAER_LITXA
AC P56264;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Caerulein.
OS Litoria xanthonera (Orange-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCB1_TaxID=79697;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97374000; PubMed=9230483;
RA Steinbörner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RAMSAY S.L.;
RT "New caerin antibacterial peptides from the skin glands of the
RT Australian tree frog Litoria xanthonera.";
RL J. Pept. Sci. 3:181-185(1997).
CC -1- FUNCTION: Hypotensive neuro-peptide.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; 1.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 10 10 AMIDATION.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1290 MW; 99DBF3837861BB5A CRC64;

Query Match 29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
DB 5 TGW 7

RESULT 6
HTF HELZE
ID -HTF HELZE STANDARD; PRT; 10 AA.
AC P16353;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrihaloaemic hormone (Hez-HRTH).
OS Heliothis zea (Corn earworm) (Bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCB1_TaxID=7113;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=88326324; PubMed=3415690;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Bird T.G.,
Tseng C.M., Zhang Y.S., Hayes D.K.;
RT "Isolation and primary structure of a neuro-peptide hormone from
RT Heliothis zea with hypertrihaloaemic and adipokinetic activities.";
RL Biochem. Biophys. Res. Commun. 155:344-350(1988).
CC -1- FUNCTION: Hypertrihaloaemic factors are neuro-peptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR: A31571; A31571.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuro-peptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1096 MW; 8E70367865A5B9D1 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
DB 3 TFSSGW 8

RESULT 7
CA31_LITCI
ID -CA31_LITCI STANDARD; PRT; 11 AA.
AC P82089;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.1/3.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCB1_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -1- FUNCTION: Hypotensive neuro-peptide (Probable).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
CC sulfated.
CC -1- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro: IPR001651; Gastrin.
DR PROSITE: PS00259; GASTRIN; FALSE NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 29.1%; Score 16; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
DB 6 TGW 8

RESULT 8
CA32_LITCI
ID -CA32_LITCI STANDARD; PRT; 11 AA.
AC P82090;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.2/3.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCB1_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RX

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT contains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."; 12 AA.
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 3.2v4 differs from isoform 3.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1 SULFATION.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;
 Query Match 29.1%; Score 16; DB 1; Length 11;
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 8 TAW 10
 Db 6 TCM 8

RESULT 9
 CXAL CONTM
 ID CXAL CONIM STANDARD; PRT; 12 AA.
 AC P50983;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin ImI.
 OS Conus imperialis (Imperial cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=35631;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Venom;
 RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
 RA Gray W.R., Olivera B.M.;
 RT "A nicotinic acetylcholine receptor ligand of unique specificity,
 RT alpha-conotoxin ImI.";
 RL J. Biol. Chem. 269:16733-16739(1994).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=95379776; PubMed=7651351;
 RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
 RA McIntosh J.M.;
 RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
 RT acetylcholine receptor blockade: preferential inhibition of homomeric
 RT alpha 7 and alpha 9 receptors";
 RL Mol. Pharmacol. 48:194-199(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99212205; PubMed=10194298;
 RA Rogers J.P., Luginbuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
 RA Wenner D.E.;
 RT "NMR solution structure of alpha-conotoxin ImI and comparison to
 RT other conotoxins specific for neuronal nicotinic acetylcholine
 RT receptors.";
 RL Biochemistry 38:3874-3882(1999).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99280313; PubMed=10350614;

RA Gouda H., Hirono S.;
 RT "Solution structure of alpha-conotoxin ImI determined by
 RT two-dimensional NMR spectroscopy."; 12 AA.
 RL Biochim. Biophys. Acta 1431:384-394(1999).
 RN [5]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99158061; PubMed=10050774;
 RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
 RA Methfessel C., Tsetlin V.I., Arseniev A.S.;
 RT "NMR spatial structure of alpha-conotoxin ImI reveals a common
 RT scaffold in snail and snake toxins recognizing neuronal nicotinic
 RT acetylcholine receptors.";
 RL FEBS Lett. 444:275-280(1999).
 RN [6]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99358772; PubMed=10431825;
 RA Lamchanh H., Jegou-Matheron C., Sarvent D., Menez A., Lancelin J.-M.;
 RT "Minimal conformation of the alpha-conotoxin ImI for the alpha7
 RT neuronal nicotinic acetylcholine receptor recognition: correlated CD,
 RT NMR and binding studies.";
 RL FEBS Lett. 454:293-298(1999).
 RN [7]
 RP STRUCTURE BY NMR.
 RX MEDLINE=10395477; PubMed=10395477;
 RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
 RT "Solution structure of alpha-conotoxin ImI by 1H nuclear magnetic
 RT resonance.";
 RL J. Med. Chem. 42:2364-2372(1999).
 RN [8]
 RP MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE
 RP THREE MUTANTS.
 RX MEDLINE=20574023; PubMed=11124036;
 RA Rogers J.P., Luginbuhl P., Pemberton K., Harty P., Wenner D.E.,
 RA Stevens R.C.;
 RT "Structure-activity relationships in a peptidic alpha7 nicotinic
 RT acetylcholine receptor antagonist.";
 RL J. Mol. Biol. 304:911-926(2000).
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
 CC inhibit them. It is highly active against the neuromuscular
 CC receptor in frog but not in mice. In contrast, it induces seizures
 CC when injected centrally in mice and rats. It targets neuronal
 CC nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors
 CC with the highest apparent affinity and homomeric alpha-9 receptors
 CC with 8-fold lower affinity. It has no effect on receptors composed
 CC of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,
 CC alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
 CC family.
 DR PIR; A53709; A53709.
 DR PDB; 1CNL; 27-MAY-99.
 DR PDB; 1E74; 27-DEC-00.
 DR PDB; 1E75; 27-DEC-00.
 DR PDB; 1E76; 27-DEC-00.
 DR PDB; 1G2G; 08-NOV-00.
 DR PDB; 1IM1; 15-JUN-99.
 DR PDB; 1IMI; 23-APR-99.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 12
 FT MOD_RES 12 12
 FT MUTAGEN 5 5
 FT MUTAGEN 7 7
 FT MUTAGEN 11 11
 FT HELIX 2 4
 FT HELIX 6 8
 FT TURN 10 12
 SQ SEQUENCE 12 AA; 1357 MW; 9C29CEA545A4176A CRC64;
 Query Match 29.1%; Score 16; DB 1; Length 12;

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Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 7 RCWA 10

RESULT 10
NO40 SESRO STANDARD; PRT; 12 AA.
AC O24369;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
OC NCBI_TaxID=3895;
CX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Stem nodules;
RC MEDLINE=98281575; PubMed=9620265;
RA Corich V., Goornachtig S., Llaevens S., van Montagu M., Holsters M.;
RT "Patterns of ENOD40 gene expression in stem-borne nodules of Sesbania
rostrata.";
RL Plant Mol. Biol. 37:67-76(1998).
CC -!- FUNCTION: Modulates the action of auxin, and may function as plant
growth regulator that alters phytohormone responses (By
similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in the early stages of the nodule
development.
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CC EMBL; Y12714; CAA73252.1; -.
DR NCBI_TaxID=3895;
KW Nodulation.
SQ SEQUENCE 12 AA; 1418 MW; 3C6955187CB326C3 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 1 MKLCW 5

RESULT 11
NO40 SOYBN STANDARD; PRT; 12 AA.
AC P55960;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early nodulin 40.
GN ENOD40.
OS Glycine max (soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OC NCBI_TaxID=3847;
CX [1]
RN SEQUENCE FROM N.A.
RP
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RC STRAIN=cv. Williams;
RX MEDLINE=94035161; PubMed=8220464;
RA Yang W.C., Katinakis P., Hendriks P., Smolders A., de Vries F.,
RA Spee J., van Kammen A., Bisseling T., Franssen H.;
RT "Characterization of GmENOD40, a gene showing novel patterns of cell-
specific expression during soybean nodule development.";
RL Plant J. 3:573-585(1993).
CC -!- FUNCTION: Modulates the action of auxin, and may function as plant
growth regulator that alters phytohormone responses (By
similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in the early stages of the nodule
development.
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC EMBL; X69154; -. NOT_ANNOTATED_CDS.
DR NCBI_TaxID=10116;
KW Nodulation.
SQ SEQUENCE 12 AA; 1391 MW; 3C6958AE78B1A733 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 40.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITTV 6
Db 5 WLITI 9

RESULT 12
UH03 RAT STANDARD; PRT; 12 AA.
AC P56572;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
CX [1]
RN SEQUENCE.
RP STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 8.3, its MW is: 28 kDa.
CC UNSURE 2 2
FT NON TER 9 9
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1255 MW; 46F58D101DC33053 CRC64;

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTUKTA 9
Db 4 TKIKVA 9

RESULT 13
V25K WSSV STANDARD; PRT; 12 AA.
ID V25K WSSV
AC P82004;
DT 16-OCT-2001 (Rel. 40, Created)
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 25 kDa structural polyprotein (Fragment).
 OS White spot syndrome virus (WSSV).
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
 OX NCBI_TaxID=92652;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=South Carolina;
 RX MEDLINE=20214217; PubMed=10752552;
 RA Wang Q., Poulos B.T., Lightner D.V.;
 RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus";
 RT Arch. Virol. 145:263-274 (2000).
 RL Arch. Virol. 145:263-274 (2000).
 CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;
 Query Match 29.1%; Score 16; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 FITTVKTA 9
 DB 5 FTLSVVT 12
 RESULT 14
 ID NEJ2_FASHE STANDARD; PRT; 14 AA.
 AC P80526;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Newly excysted juvenile protein 2 (Fragment).
 OS Fasciola hepatica (Liver fluke).
 CC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 CC Echinostomida; Echinostomata; Fasciolidae; Fasciolidae; Fasciola.
 OX NCBI_TaxID=6192;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95366993; PubMed=7639732;
 RA Tkalcic J., Asman K., Meusen E.;
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile proteins";
 RL Biochem. Biophys. Res. Commun. 213:169-174 (1995).
 CC -!- DEVELOPMENTAL STAGE: Expressed at the newly excysted juvenile stage.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1581 MW; 9B0F0090CC8C0DF1 CRC64;
 Query Match 29.1%; Score 16; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 5.1e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 KTAW 10
 DB 6 RTHW 9
 RESULT 15
 ID RT34_BOVIN STANDARD; PRT; 8 AA.
 AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
 GN MRPS34.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Liver;
 RX MEDLINE=21276436; PubMed=11279123;
 RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome: identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374 (2001).
 CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;
 Query Match 27.3%; Score 15; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 AW 10
 DB 1 AW 2
 RESULT 16
 ID LMIP_LOCMI STANDARD; PRT; 9 AA.
 AC P31799;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Locustamycininhibiting peptide (LOM-MIP).
 OS Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92179466; PubMed=1796179;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, identification and synthesis of locustamycininhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locusta migratoria.";
 RL Locusta migratoria.;
 RL Regul. Pept. 36:111-119 (1991).
 CC -!- FUNCTION: Suppresses spontaneous contractions of the hindgut and oviduct.
 CC -!- TISSUE SPECIFICITY: Neurons located in two ventral cell clusters in the suboesophageal ganglion.
 DR PIR; A60065; AKLQIM.
 KW Amidation; Neuropeptide.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;
 Query Match 27.3%; Score 15; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 AW 10
 DB 1 AW 2
 RESULT 17
 ID TKNK_PIG STANDARD; PRT; 10 AA.
 AC P01292;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurokinin B (NKB) (Neuromedin K).


```
GN TAC3 OR NKNB.
OS Sus scrofa (Pig), and
OC Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823, 8406;
RN [1]
RN SEQUENCE
RP SPECIES=Pig; TISSUE=Spinal cord;
RC MEDLINE=83282812; PubMed=6576785;
RA Kangawa K., Minamino N., Fukuda A., Matsuo H.;
RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
RN spinal cord.";
RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
RN [2]
RN SEQUENCE.
RP SPECIES=R. ridibunda; TISSUE=Brain;
RC MEDLINE=92044543; PubMed=1658233;
RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
RN neurokinin B from the brain of the frog Rana ridibunda.";
RL J. Neurochem. 57:2086-2091(1991).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy Neurokinin.
DR PIR; A01560; SPPGKN.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1211 MW; E1FA7C62C9C9CAA1 CRC64;
SQ
Query Match 27.3%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFI 3
Db 5 FFV 7
RESULT 18
ID TPIS_NICPL STANDARD; PRT; 10 AA.
AC P19118;
DT 01-NOV-1990 (Rel. 16, Created)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana plumbaginifolia (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OC NCBI_TaxID=4092;
RN [1]
RN SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electroblotted from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-
CC phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- MISCELLANEOUS: In plants, there are two types of TPIS, cytosolic
CC and plastid.
CC -!- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR PIR; A27617; A27617.
DR
InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
Pentose shunt.
FT NON_TER 10
FT SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;
SQ
Query Match 27.3%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFI 3
Db 4 FFV 6
RESULT 19
ID YZPY_ECOLI STANDARD; PRT; 12 AA.
AC P17776;
DT 01-AUG-1990 (Rel. 15, Created)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85003588; PubMed=6207018;
RA Poulsen P., Bonekamp F., Jensen K.F.;
RT "Structure of the Escherichia coli pyre operon and control of pyre
RN expression by a UTP modulated intergenic attenuation.";
RL EMBO J. 3:1783-1790(1984).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=83287414; PubMed=6349999;
RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,
RA Lundberg L.G.;
RT "Nucleotide sequence of the Escherichia coli pyre gene and of the DNA
RN in front of the protein-coding region.";
RL Eur. J. Biochem. 135:223-229(1983).
CC -!- CAUTION: This sequence, according to the EcoSeq database (K. Rudd)
CC is probably not a real protein; therefore this entry will probably
CC be deleted in future releases.
CC -----
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CC -----
DR EMBL; X00781; -; NOT ANNOTATED_CDS.
DR EMBL; V01578; -; NOT ANNOTATED_CDS.
DR PIR; A30400; LFECPE.
KW Hypothetical protein.
SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;
Query Match 27.3%; Score 15; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FFI 3
Db 5 FFV 7
RESULT 20
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BI21 LITRU
ID E121 LITRU STANDARD; PRT; 13 AA.
AC P82097;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1599 MW; C1808EF326F57322 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTAW 10
DB 5 KVKW 8

RESULT 21
BI22 LITRU
ID E122 LITRU STANDARD; PRT; 13 AA.
AC P82098;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Electrin 2.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 13
SQ SEQUENCE 13 AA; 1598 MW; C1808EF33B357322 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KTAW 10
DB 5 KVKW 8

RESULT 22
UHA3_CANFA

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ID UHA3 CANFA STANDARD; PRT; 13 AA.
AC P56535;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 7520) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.9, its MW is: 55.4 kDa.
DR HSC-2DPAGE; P56535; DOG.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1457 MW; 9F5BD94B9306D76A CRC64;

Query Match 27.3%; Score 15; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FIT 4
DB 3 FIT 5

RESULT 23
ALYT_ALYOB
ID ALYT ALYOB STANDARD; PRT; 14 AA.
AC P08944;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alytesin.
OS Alytes obstetricans (Midwife toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Discoglossidae; Alytes.
OX NCBI_TaxID=8443;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=84131098; PubMed=6141890;
RA Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
RT "Active peptides in the skins of one hundred amphibian species from
RT Australia and Papua New Guinea.";
RL Comp. Biochem. Physiol. 77C:99-108(1984).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin
CC family.
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 14
SQ SEQUENCE 14 AA; 1554 MW; D3C4E4D3AF129666 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 14;
Best Local Similarity 66.7%; Pred. No. 7.9e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
DB 6 TOW 8

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RESULT 24
LFP2_ECOLI
ID LFP2_ECOLI STANDARD; PRT; 14 AA.
AC P06985;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phenylalanyl-tRNA synthetase operon leader peptide (PheST attenuator
peptide).
GN PHM OR PHTL OR B1715 OR C5495 OR Z2744 OR ECS2422 OR STYL1774 OR TL1217
GN OR SF1516 OR S4806.
OS Escherichia coli, O6.
OS Escherichia coli, O6.
OS Escherichia coli O157:H7,
OS Salmonella typhi, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia
OX NCBI_TaxID=562, 217992, 83334, 601, 623;
[1]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=85210878; PubMed=3158742;
RA Springer M., Mayaux J.-F., Fayat G., Plumbridge J.A., Graffe M.,
RA Blanquet S., Grunberg-Manago M.;
RT "Attenuation control of the Escherichia coli phenylalanyl-tRNA
synthetase operon.";
RL J. Mol. Biol. 181:467-478 (1985).
[2]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=84090239; PubMed=6317865;
RA Fayat G., Mayaux J.-F., Sacerdot C., Fromant M., Springer M.,
RA Grunberg-Manago M., Blanquet S.;
RT "Escherichia coli phenylalanyl-tRNA synthetase operon region.
RT Evidence for an attenuation mechanism. Identification of the gene for
the ribosomal protein L20.";
RL J. Mol. Biol. 171:239-261 (1983).
[3]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=88163794; PubMed=3126825;
RA Springer M., Graffe M., Mayaux J.-F., Dardel F., Fayat G.,
RA Blanquet S., Grunberg-Manago M.;
RT "Open reading frames in the control regions of the phenylalanyl-tRNA
synthetase operon of E. coli.";
RL Biochimie 69:1065-1070 (1987).
[4]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
[5]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6.H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Weich R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
[6]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
[7]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
[8]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
[9]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodyanni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337 (2003).
[10]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441 (2002).
[11]
RN
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786 (2003).
CC
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CC -----
 DR EMBL; M10423; ARA23961.1; -
 DR EMBL; V00291; ARA23963.1; -
 DR EMBL; M13251; ARA24333.1; -
 DR EMBL; AE000266; AAC74785.1; -
 DR EMBL; AE016761; AAN80571.1; -
 DR EMBL; AE005394; AAG56702.1; -
 DR EMBL; AP002558; BAB35845.1; -
 DR EMBL; AL627271; CAD02016.1; -
 DR EMBL; AE016838; AAO68872.1; -
 DR EMBL; AE015174; AAN43106.1; -
 DR EMBL; AE016983; AAP16996.1; -
 DR PIR; B85780; B85780.
 DR PIR; F90931; F90931.
 DR PIR; S11551; LFECS.
 DR Ecogen; Egl1272; pheM.
 KW Leader peptide; Complete proteome.
 SQ SEQUENCE 14 AA; 1762 MW; 7D31C48E0060F0D4 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 7.9e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFITV 5
 : :
 Db 10 FVFST 14

RESULT 25
 UC04 MAIZE
 ID UC04 MAIZE STANDARD; PRT; 14 AA.
 AC P80610;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 128) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Tournet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 Fernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.8, its MW is: 34.6 kDa.
 CC Maize-ZDPAGE; P80610; COLEOPTILE.
 DR MaizedB; 123926; -
 FT NON TER 1 14
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1393 MW; C14451BA1116D4AD CRC64;

Query Match 27.3%; Score 15; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVK 7
 : :
 Db 5 FSAIVR 10

RESULT 26
 PLP BRANA
 ID PLP BRANA STANDARD; PRT; 8 AA.
 AC P81707;

DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Plastidial lipid-associated protein (Fragment).
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. TOPAZ; TISSUE=Tapetum;
 RX MEDLINE=99349136; PubMed=10420651;
 RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
 Murphy D.J.;
 RT "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of Brassica napus."
 RL Planta 208:588-598(1999).
 CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-specific plastidial lipid organelle.
 CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
 FT NON TER 8
 SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
 : :
 Db 1 VIDVNDWE 8

RESULT 27
 PORD_METTM
 ID PORD_METTM STANDARD; PRT; 12 AA.
 AC P80903;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase delta chain) (POR) (Pyruvate-ferredoxin oxidoreductase delta subunit) (Fragment).
 DE PORD.
 GN PORD.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97261844; PubMed=9108258;
 RA Tersteegen A., Linder D., Thauer R.K., Hedderich R.;
 RT "Structures and functions of four anabolic 2-oxoacid oxidoreductases in Methanobacterium thermoautotrophicum."
 RL Eur. J. Biochem. 244:862-868(1997).
 CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-CoA + CO(2) + reduced ferredoxin.
 CC -!- COFACTOR: Binds 2 4Fe-4S clusters (By similarity).
 CC -!- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one gamma chain.
 CC -!- MISCELLANEOUS: Has a pH optimum of 10.0 and an optimal temperature of 80 degrees Celsius.
 CC -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
 KW Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1241 MW; 2D5406SD1BD1ADD8 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TVK 7
 : :
 Db 1

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Db          7 TVK 9

RESULT 28
ID YPNP_PHOLU STANDARD; PRT; 13 AA.
AC P41122;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in pnp 3' region (ORF3) (Fragment).
OS Photorhabdus luminescens (Xenorhabdus luminescens).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=29488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K122;
RX MEDLINE=94266731; PubMed=8206856;
RA Clarke D.J., Dowds B.C.A.;
RT "The gene coding for polynucleotide phosphorylase in Photorhabdus sp.
RL strain K122 is induced at low temperatures.";
RL J. Bacteriol. 176:3775-3784(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X76069; CAA53672.1; -
CC DR Hypothetical protein.
CC KW Hypothetical protein.
CC FT NON_TER 13
CC SQ SEQUENCE 13 AA; 1634 MW; 64774A4F6267A364 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
   ||:
Db 3 FFL 5

RESULT 29
ID CXIA_CONBE STANDARD; PRT; 14 AA.
AC P58623;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conotoxin BcXia.
OS Conus betulinus (Beech cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89764;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20058566; PubMed=10591037;
RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;
RT "Studies on conotoxins of Conus betulinus.";
RL J. Nat. Toxins 8:341-349(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -|- MASS SPECTROMETRY: MW=1589.3; METHOD=WALDI.
CC -|- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.
KW Neurotoxin; Toxin.
FT DISULFID 1 9 PROBABLE.
FT DISULFID 2 12 PROBABLE.

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FT DISULFID 6 13 PROBABLE.
SQ SEQUENCE 14 AA; 1597 MW; 95B725AA93432EB1 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 14;
Best Local Similarity 28.6%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 TTVKTAW 10
   ||:|
Db 8 TCMPCCW 14

RESULT 30
ID LPW_CITFR STANDARD; PRT; 14 AA.
AC P03056;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83007061; PubMed=6749821;
RA Blumenberg M., Yanofsky C.;
RT "Evolutionary divergence of the Citrobacter freundii tryptophan
RL operon regulatory region: comparison with other enteric bacteria.";
RL J. Bacteriol. 152:57-62(1982).
CC -|- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J01557; -; NOT_ANNOTATED_CDS.
CC DR PIR; A03592; LFEWMC.
CC KW Tryptophan biosynthesis; Leader peptide.
CC SQ SEQUENCE 14 AA; 1720 MW; 5B792A473B8048E7 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TTVKTAW 10
   ||:|
Db 4 TTVLHGW 10

RESULT 31
ID LPW_ECOLI STANDARD; PRT; 14 AA.
AC P03053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR TRPE OR B1265 OR C5494 OR Z2545 OR ECS1837 OR SF1268 OR
GN S4805.
OS Escherichia coli,
OS Escherichia coli O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=82150258; PubMed=7038627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RW Horowitz H., van Cleemput M., Wu A.M.;
RT "The complete nucleotide sequence of the tryptophan operon of
RT Escherichia coli.";
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RW Yanofsky C.;
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT Escherichia coli.";
RL J. Mol. Biol. 103:351-381(1976).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.;
RW "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RT secondary structure involving the tryptophan codon region.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RW Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RW Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RW Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RW Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RW Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Probst G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RW Grobbeck E.J., Davis N.W., Lim A., Dimallanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RW Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RW Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RW Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RW Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RW Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RW Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RW Pournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RW Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
RN [10]
RP FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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CC
CC EMBL: J01714; AAA57296.1; -
CC EMBL: A04494; CRA00361.1; -
CC EMBL: AE000224; AAC74347.1; -
CC EMBL: AE016760; AAN80196.1; -
CC EMBL: AE005380; AAG56550.1; -
CC EMBL: AP002556; BAB35260.1; -
CC EMBL: AE015153; AAN42881.1; -
CC EMBL: AE016982; AAP16766.1; -
CC PIR: A03589; LFECW.
CC PIR: B85761; B85761.
CC PIR: E90858; E90858.
CC EcoGene; EG11274; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1723 MW; 5B79306BE804A37 CRC64;
Query Match 25.5%; Score 14; DB 1; Length 14;
Best Local Similarity 37.5%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 ITTVKTAW 10
Db 4 IFVLGWW 11
RESULT 32
AKH TABAT
ID AKH TABAT STANDARD; PRT; 8 AA.
AC P14595;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
(DCC I).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;

RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).
 CC -!- FUNCTION: This hormone, released from cells in the corpora
 CC cardiaca after the beginning of flight, causes release of
 CC diglycerides from the fat body and then stimulates the flight
 CC muscles to use these diglycerides as an energy source.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
 DR PIR; A33995; A33995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE; PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 5 TVKTAW 10
 Db 3 TTFPGW 8
 RESULT 33
 LCK2 LEUMA
 ID LCK2 LEUMA STANDARD; PRT; 8 AA.
 AC P21141;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin II (L-II).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of two neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT Cephalomyotopins.";
 RL Comp. Biochem. Physiol. 84C:205-211 (1986).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach protodeum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 852 MW; DC6365A5B9C8676A CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 8 TAW 10
 Db 5 SSW 7
 RESULT 34
 LCK5 LEUMA
 ID LCK5 LEUMA STANDARD; PRT; 8 AA.
 AC P19987;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin V (L-V).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotropic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30 (1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach protodeum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0315; JS0315.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 784 MW; 736365A5B9C865B8 CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 8 TAW 10
 Db 5 SSW 7
 RESULT 35
 LCK7 LEUMA
 ID LCK7 LEUMA STANDARD; PRT; 8 AA.
 AC P19989;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin VII (L-VII).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OC NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 RT VIII: the final members of this new family of cephalomyotropic
 RT peptides isolated from head extracts of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:31-34 (1987).
 CC -!- FUNCTION: This cephalomyotropic peptide stimulates contractile
 CC activity of cockroach protodeum (hindgut).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0317; JS0317.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9C8676A CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 8 TAW 10
 Db 5 SSW 7
 RESULT 36
 APE CAPGI
 ID APE CAPGI STANDARD; PRT; 10 AA.

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AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RX STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
RT factor.";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
CC TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: Requires magnesium or calcium.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 VKTAW 10
DB 2 VNNLW 6

RESULT 37
COXQ SHEEP STANDARD; PRT; 10 AA.
ID COXQ SHEEP STANDARD; PRT; 10 AA.
AC P80337;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart, and Liver;
RA Freund R., Kadenbach B.;
RL Submitted (MAR-1994) to Swiss-Prot.
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1027 MW; C4E95CA33DC7633D CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTA 9
DB 2 TAKPA 6

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RESULT 38
HTF_TABAT STANDARD; PRT; 10 AA.
ID HTF_TABAT STANDARD; PRT; 10 AA.
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DE (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RX TISSUE=Corpora cardiaca;
RX MEDLINE=90046758; PubMed=2813385;
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT flies (Diptera).";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC PIR; B33995; B33995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.4e+04;
Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TVKTAW 10
DB 3 TETPCW 8

RESULT 39
UR2 POLSP STANDARD; PRT; 12 AA.
ID UR2 POLSP STANDARD; PRT; 12 AA.
AC P81022;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin II (U-II) (UII).
OS Polyodon spathula (North American paddlefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Chondrostei; Acipenseriformes; Polyodontidae;
OC Polyodon.
OX NCBI_TaxID=7913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=96051494; PubMed=8536944;
RA Waugh D., Youson J., Mims S.D., Sower S., Conlon J.M.;
RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT spathula).";
RL Gen. Comp. Endocrinol. 99:323-332(1995).
CC -!- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.

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CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the urotensin 2 family.
 DR InterPro: IPR001483; Urotensin_II.
 DR Pfam: PF02083; Urotensin_II; 1.
 DR PROSITE: PS00984; UROTENSIN_II; 1.
 KW Hormone.
 FT DISULFID 6 11 BY SIMILARITY.
 SQ SEQUENCE 12 AA; 1410 MW; 7551E9DBB879CEBB CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 12;
 Best Local Similarity 28.6%; Pred. No. 1.6e+04;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 4 TTVKAW 10
 : : :
 Db 2 STSECFW 8
 RESULT 40
 LIGB TRAVE STANDARD; PRT; 13 AA.
 AC P20012;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ligninase B (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
 peroxidase) (Fragment).
 OS Trametes versicolor (White-rot fungus).
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 CC Aphyllophorales; Trametes.
 OX NCBI_TaxID=5325;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89211432; PubMed=2707445;
 RA Jonsson L., Karlsson O., Lundquist K., Nyman P.O.;
 RT "Trametes versicolor ligninase: isozyme sequence homology and
 substrate specificity."
 RL FEBS Lett. 247:143-146(1989).
 CC -!- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-
 C(beta) cleavage of the propyl side chains of lignin.
 CC -!- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,3-diol +
 H(2)O(2) = veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol
 + 4 H(2)O.
 CC -!- PATHWAY: Lignin degradation; first step.
 CC -!- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
 DR PIR: S04014; S04014.
 DR InterPro: IPR002016; Peroxidase.
 DR PROSITE: PS00435; PEROXIDASE_1; PARTIAL.
 DR PROSITE: PS00436; PEROXIDASE_2; PARTIAL.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
 KW Multigene family; Lignin degradation.
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1269 MW; 22C50B5872A52C8 CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 VKTA 9
 : : :
 Db 7 VNTA 10
 RESULT 41
 TY13_PHYO STANDARD; PRT; 13 AA.
 AC P04096;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1986 (Rel. 03, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tyrotyllylin-13.
 OS Phyllomedusa rohdei (Rohde's leaf frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8394;
 RN [1]
 RP SEQUENCE.
 RA Montecucchi P.C., Gozzini L., Erspamer V.;
 RT "Primary structure determination of a tryptophan-containing
 tridecapeptide from Phyllomedusa rohdei.";
 RL Int. J. Pept. Protein Res. 27:175-182(1986).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR: A05174; A05174.
 KW Amphibian defense peptide; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 KTAW 10
 : : :
 Db 3 KPYW 6
 RESULT 42
 KARA BROPL STANDARD; PRT; 14 AA.
 ID P22442;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Karatin (EC 3.4.22.-) (Fragment).
 OS Bromelia plumieri (Karatas).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Bromeliaceae;
 CC Bromelia.
 OX NCBI_TaxID=4617;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90344224; PubMed=1368518;
 RA Montes C., Amador M., Cuevas D., Cordoba F.;
 RT "Subunit structure of karatinin, the proteinase isolated from
 Bromelia plumieri (karatas).";
 RL Agric. Biol. Chem. 54:17-24(1990).
 CC -!- SUBUNIT: Dimer of two small subunits linked by disulfide bonds.
 CC -!- SIMILARITY: Belongs to peptidase family C1.
 DR PIR: PT0029; PT0029.
 DR InterPro: IPR000169; SHprot acsite.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; PARTIAL.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; PARTIAL.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN; PARTIAL.
 KW Hydrolase; Thiol protease.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1602 MW; FDA156893F0834FA CRC64;
 Query Match 23.6%; Score 13; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 1.8e+04;
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 6 VKTAW 10
 : : :
 Db 1 VPETW 5
 RESULT 43
 MCRX_METTM STANDARD; PRT; 14 AA.
 ID P58815;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Methyl-coenzyme M reductase II alpha subunit (EC 1.8.-.-) (MCR II

DE alpha) (Fragment).
GN MRTA.
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=79929;
RN [1]_SEQUENCE
RX MEDLINE=91099370; PubMed=2269306;
RA Robert S., Linder D., Ellermann J., Thauer R.K.;
RT "Two genetically distinct methyl-coenzyme M reductases in
Methanobacterium thermoautotrophicum strain Marburg and Delta H.";
RL Eur. J. Biochem. 194; 871-877 (1990).
CC -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
to methane and an heterodisulfide.
CC -!- CATALYTIC ACTIVITY: CH(3)-S-COM + H-S-HTP = CH(4) + CoM-S-S-HTP.
CC -!- COFACTOR: Binds 2 coenzyme F430 noncovalently per hexamer.
CC Coenzyme F430 is a yellow nickel porphyrinoid.
CC -!- PATHWAY: Methanogenesis; last step.
CC -!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains.
CC -!- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
KW Methanogenesis; Oxidoreductase; Multigene family.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1718 MW; D317CCC562F00E29 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVK 7
| : : |
Db 7 FLKALK 12

RESULT 44
SMS_MYOSC
ID SMS1_MYOSC STANDARD; PRT; 14 AA.
AC P20750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin I.
OS Myoxocephalus scorpius (Shorthorn sculpin), (Daddy sculpin),
OS Onchorhynchus kisutch (Coho salmon), and
OS Anguilla anguilla (European freshwater eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidae; Cottidae; Myoxocephalus.
OX NCBI_TaxID=8097, 8019, 7936;
RN [1]
RP SEQUENCE.
RC SPECIES=M. scorpius; TISSUE=Pancreas;
RX MEDLINE=88029486; PubMed=2889597;
RA Conlon J.M., Davis M.S., Falkner S., Thim L.;
RT "Structural characterization of peptides derived from
prosomatostatins I and II isolated from the pancreatic islets of two
species of teleostean fish: the daddy sculpin and the flounder.";
RL Eur. J. Biochem. 168:647-652 (1987).
RN [2]
RP SEQUENCE.
RC SPECIES=O. kisutch; TISSUE=Pancreas;
RX MEDLINE=87055212; PubMed=2877919;
RA Plietskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
RA Kimmel J.R., Andrews P.C., Gorman A.;
RT "Characterization of coho salmon (Oncorhynchus kisutch) islet
somatostatins.";
RL Gen. Comp. Endocrinol. 63:252-263 (1986).
RN [3]
RP SEQUENCE.

RC SPECIES=A. anguilla; TISSUE=Pancreas;
RX MEDLINE=89065329; PubMed=2904391;
RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
RT "Somatostatin-related and glucagon-related peptides with unusual
structural features from the European eel (Anguilla anguilla).";
RL Gen. Comp. Endocrinol. 72:181-189 (1988).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatostatin family.
DR PIR; A60840; A60840.
DR PIR; B60842; B60842.
DR PIR; S00172; S00172.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Hormone; Multigene family.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PFITT 5
| | |
Db 6 FFWKT 10

RESULT 45
SMS_ALLMI
ID SMS_ALLMI STANDARD; PRT; 14 AA.
AC P31885;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Somatostatin-14.
OS Alligator mississippiensis (American alligator), and
OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496, 34903;
RN [1]
RP SEQUENCE.
RC SPECIES=A. mississippiensis; TISSUE=Stomach;
RX MEDLINE=93324451; PubMed=8101369;
RA Wang Y., Conlon J.M.;
RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
and stomach of the alligator.";
RL Peptides 14:573-579 (1993).
RN [2]
RP SEQUENCE.
RC SPECIES=T. scripta;
RX MEDLINE=90341082; PubMed=1974347;
RA Conlon J.M., Hicks J.W.;
RT "Isolation and structural characterization of insulin, glucagon and
somatostatin from the turtle, Pseudemys scripta.";
RL Peptides 11:461-466 (1990).
CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the somatostatin family.
DR PIR; C60414; C60414.
DR InterPro; IPR004250; Somatostatin.
DR Pfam; PF03002; Somatostatin; 1.
KW Hormone.
FT DISULFID 3 14
SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 PFITT 5
| | |
Db 6 FFWKT 10

Search completed: August 30, 2004, 10:50:25
Job time : 3.72297 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 3.00676 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFITVKTAW 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	38.2	13	2 B56864	dipeptidyl-peptida
2	20	36.4	9	2 I46016	cytochrome-c
3	18	32.7	12	2 I77529	cytochrome-c
4	18	32.7	13	2 A59491	epithelial dog all
5	18	32.7	14	2 PT0259	Ig heavy chain CRD
6	18	32.7	14	2 PH1347	Ig heavy chain DJ
7	17	30.9	8	2 A59028	MHC class I histoc
8	17	30.9	11	2 S54347	tubulin beta chain
9	17	30.9	11	2 A49037	TcR gamma V-J regi
10	17	30.9	11	2 B49037	TcR gamma V-J regi
11	17	30.9	11	2 C49037	TcR gamma V-J regi
12	17	30.9	12	2 I64929	gene HEXA protein
13	17	30.9	12	2 PH1675	Ig heavy chain V r
14	17	30.9	13	2 PH1676	Ig heavy chain V r
15	17	30.9	13	2 S70723	lipamide dehydrog
16	17	30.9	14	2 PH1677	Ig heavy chain V r
17	17	30.9	14	2 PH1705	Ig heavy chain V r
18	17	30.9	14	2 S62374	alpha-1-antichymot
19	17	30.9	14	2 PH1625	Ig H chain V-D-J r
20	16	29.1	8	2 A28004	adipokinetic hormo
21	16	29.1	9	2 A24244	adipokinetic hormo
22	16	29.1	9	2 A61357	phylliscoerulein -
23	16	29.1	9	2 A43848	cell surface adhes
24	16	29.1	10	2 A31571	hypertrehalosemic/
25	16	29.1	10	2 A61337	caerulein - frog (
26	16	29.1	12	1 A53709	alpha-conotoxin Im
27	16	29.1	13	2 PC2369	unidentified 85K p
28	16	29.1	13	2 B19434	probable sex-speci
29	16	29.1	14	2 PH1627	Ig H chain V-D-J r

30 15 27.3 9 1 AKLQIM
31 15 27.3 9 2 C57444
32 15 27.3 9 2 D57444
33 15 27.3 9 2 A28924
34 15 27.3 9 2 PT0634
35 15 27.3 10 1 SPPGNK
36 15 27.3 10 2 S66248
37 15 27.3 10 2 A27617
38 15 27.3 10 2 PN0165
39 15 27.3 10 2 A35556
40 15 27.3 10 2 TL3838
41 15 27.3 10 2 TL3976
42 15 27.3 10 2 TL7057
43 15 27.3 10 2 TL2303
44 15 27.3 10 2 TL4019
45 15 27.3 10 2 TL7060

ALIGNMENTS

RESULT 1

B56864
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
C:Accession: B56864

R;Plakidou-Dymock, S.; McGivan, J.D.
Biochim. Biophys. Acta 1145, 105-112, 1993

A:Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border mem

A:Reference number: A56864; MUID:93136203; PMID:8093665

A:Accession: B56864

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <PLA>

A:Experimental source: renal brush-border membrane vesicles

C:Keywords: dipeptidylpeptide hydrolase

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10

DB 1 MKTPW 5

RESULT 2

I46016
cytochrome-c - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C:Accession: I46016
R;Blessing, M.; Jorcano, J.L.; Franke, W.W.
EMBO J. 8, 117-126, 1989

A:Title: Enhancer elements directing cell-type-specific expression of cytochrome-c

A:Reference number: I46016; MUID:89231609; PMID:2469572

A:Accession: I46016

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-9 <BLE>

A:Cross-references: EMBL:X14478; NID:g303; PIDN:CAA32640.1; PID:g577897

Query Match 36.4%; Score 20; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTVKT 8

DB 5 STVKT 9

RESULT 3

I77529

estrogen receptor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I77529
R:Wang, Y.; Miksicak, R.J.
Mol. Endocrinol. 5, 1707-1715, 1991
A:Title: Identification of a dominant negative form of the human estrogen receptor.
A:Reference number: 157707; PMID:92140401; PMID:1779972
A:Accession: I77529
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:S79911; NID:g244433; PIDN:AA821301.1; PID:g244434
C:Keywords: steroid hormone receptor

Query Match 32.7%; Score 18; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVTKTAW 10
: || ||
DB 2 SVTKAW 7

RESULT 4

A59491
epithelial dog allergen - Canis familiaris (fragment)
C:Species: Canis familiaris
C>Date: 27-Oct-2003 #sequence_revision 27-Oct-2003 #text_change 27-Oct-2003
C:Accession: A59491
R:Saarelainen, S.; Taivainen, A.; Rytikm-vnen-Nissinen, M.; Auriola, S.; Immonen, A.; MW-
submitted to the Protein Sequence Database, October 2003
A:Description: Diagnosis of dog allergy with recombinant allergens.
A:Reference number: A59491
A:Accession: A59491
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <VIR>
A>Note: IGE-binding protein; allergen

Query Match 32.7%; Score 18; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
: || ||
DB 5 LTQVSGPW 12

RESULT 5

PT0259
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0259
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; PMID:91108337; PMID:1899102
A:Accession: PT0259
A:Molecule type: DNA
A:Residues: 1-14 <VAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.7%; Score 18; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKTA 9
: || ||
DB 3 LTTIAAA 9

RESULT 6

PH1347
Ig heavy chain DJ region (clone C100-103A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1347
R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; PMID:93094761; PMID:1460419
A:Accession: PH1347
A:Molecule type: DNA
A:Residues: 1-14 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.7%; Score 18; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FITT 5
: || ||
DB 6 FLTT 9

RESULT 7

A59028
MHC class I histocompatibility antigen HLA-C alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 31-Dec-2001
C:Accession: A59028
R:Escolano, J.M.
submitted to the Protein Sequence Database, August 1998
A:Reference number: A59028
A:Accession: A59028
A:Molecule type: protein
A:Residues: 1-8 <ESC>
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen

Query Match 30.9%; Score 17; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PFITTV 6
: || ||
DB 1 YFYTAV 6

RESULT 8

S54347
tubulin beta chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999
C:Accession: S54347
R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
A:Reference number: S54343; PMID:95194333; PMID:7887910
A:Accession: S54347
A:Molecule type: protein
A:Residues: 1-11 <OKA>

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVK 7
: || ||
DB 7 IATIK 11

RESULT 9

A49037
Tcr gamma V-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49037
R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A:Reference number: A49037; MUID:92164730; PMID:1311262
A:Accession: A49037
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <EQ>
A:Cross-references: GB:S90637; NID:g246292; PIDN:AAB21549.1; PID:g246293
A:Experimental source: dendritic epidermal T-cell lines
A>Note: sequence extracted from NCBI backbone (NCBIN:90637, NCBIP:90641)

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAW 10
Db 8 TSW 10

RESULT 10
B49037
Tcr gamma V-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: B49037
R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A:Reference number: A49037; MUID:92164730; PMID:1311262
A:Accession: B49037
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <EQ>
A:Cross-references: GB:S90638; NID:g246290; PIDN:AAB21548.1; PID:g246291
A:Experimental source: dendritic epidermal T-cell lines
A>Note: sequence extracted from NCBI backbone (NCBIN:90638, NCBIP:90644)

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAW 10
Db 8 TSW 10

RESULT 11
C49037
Tcr gamma V-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: C49037
R;Ezquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A:Reference number: A49037; MUID:92164730; PMID:1311262
A:Accession: C49037
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <EQ>
A:Cross-references: GB:S90639; NID:g246292; PIDN:AAB21549.1; PID:g246293
A:Experimental source: dendritic epidermal T-cell lines
A>Note: sequence extracted from NCBI backbone (NCBIN:90639, NCBIP:90645)

Query Match 30.9%; Score 17; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAW 10
Db 8 TSW 10

RESULT 12
164829
Gene HEXA protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: 164829
R;Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A:Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A:Reference number: I51882; MUID:95193801; PMID:7887427
A:Accession: 164829
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:S76984; NID:g912781; PIDN:AAD14243.1; PID:g4261943
C:Genetics:
A:Gene: GDB:HEXA
A:Cross-references: GDB:120040; OMIM:272800
A:Map position: 15q23-15q24
C:Superfamily: beta-hexosaminidase

Query Match 30.9%; Score 17; DB 2; Length 12;
Best Local Similarity 10.0%; Pred. No. 3.9e+03;
Matches 1; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FFITTVKTAW 10
Db 2 WYLNRSILW 11

RESULT 13
PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1675
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1675
A:Molecule type: mRNA
A:Residues: 1-12 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 TAW 10
Db 2 TSW 4

RESULT 14
PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1676
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385

A:Accession: PH1676

A:Molecule type: mRNA

A:Residues: 1-13 <MCH>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10

|||

Db 2 TSW 4

RESULT 15

S70723

Lipoamide dehydrogenase homolog - Salmonella typhimurium (fragment)

C:Species: Salmonella typhimurium

C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C:Accession: S70723

R:Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A>Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophils

A:Reference number: S70719; UID:96100451; PMID:8559071

A:Accession: S70723

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <QIS>

A:Experimental source: strain SL1344

Query Match 30.9%; Score 17; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTVKT 8

|||

Db 2 TEIKT 6

RESULT 16

PH1677

Ig heavy chain V region (clone NP-6-6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1677

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; UID:93301607; PMID:8315385

A:Accession: PH1677

A:Molecule type: mRNA

A:Residues: 1-14 <MCH>

A:Experimental source: B cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10

|||

Db 2 TSW 4

RESULT 17

PH1705

Ig heavy chain V region (clone ASC-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1705

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A>Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; UID:93301607; PMID:8315385

A:Accession: PH1705

A:Molecule type: mRNA

A:Residues: 1-14 <MCH>

A:Experimental source: B cell

A>Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 12

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TAW 10

|||

Db 2 TSW 4

RESULT 18

S62374

alpha-1-antichymotrypsin - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997

C:Accession: S62374

R:Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;

Eur. J. Biochem. 235, 821-827, 1996

A>Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin variant

A:Reference number: S62374; UID:96184564; PMID:8654434

A:Accession: S62374

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-14 <TSU>

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFITTV 6

|||

Db 3 FFMSKV 8

RESULT 19

PH1625

Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1625

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; UID:93301609; PMID:8315387

A:Accession: PH1625

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 30.9%; Score 17; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKT 8

|||

Db 5 ITTRET 10

RESULT 20

A28004

adipokinetic hormone G - two-spotted cricket

N/Alternate names: AKH-G
 C/Species: Gryllus bimaculatus (two-spotted cricket)
 C/Date: 30-Jun-1989 #sequence_revision 24-Oct-1997 #text_change 24-Oct-1997
 C/Accession: A28004
 R/Gaede, G.; Rinehart, K.L.
 Biochem. Biophys. Res. Commun. 149, 908-914, 1987
 A/Title: Primary sequence analysis by fast atom bombardment mass spectrometry of a peptide
 A/Reference number: A28004; MUID:88106553; PMID:3426616
 A/Accession: A28004
 A/Molecule type: protein
 A/Residues: 1-8 <GAE>
 A/Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C/Superfamily: adipokinetic hormone
 C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F/8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
 DB 6 TGW 8

RESULT 21
 A24244
 adipokinetic hormone - bollworm
 N/Alternate names: Hez-AKH
 C/Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C/Date: 31-Mar-1988 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
 C/Accession: A24244
 R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Holman, G.M.; Wagner, R.M.; Ridgway
 Biochem. Biophys. Res. Commun. 135, 622-628, 1986
 A/Title: Isolation and primary structure of a peptide from the corpora cardiaca of Helio
 A/Reference number: A24244; MUID:86186794; PMID:3964263
 A/Accession: A24244
 A/Molecule type: protein
 A/Residues: 1-9 <JAF>
 C/Superfamily: adipokinetic hormone
 C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F/9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 TVKTAW 10
 DB 3 TFWSSW 8

RESULT 22
 A61357
 phyllocaerulein - Sauvage's leaf frog
 C/Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
 C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
 C/Accession: A61357
 R/Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
 Br. J. Pharmacol. 37, 198-206, 1969
 A/Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nona
 A/Reference number: A61357; MUID:70005484; PMID:5824931
 A/Accession: A61357
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-9 <ANA>
 C/Superfamily: Gastrin
 C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F/3/Binding site: sulfate (Tyr) (covalent) #status experimental
 F/9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
 DB 4 TGW 6

RESULT 23
 A43848
 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
 C/Species: Staphylococcus aureus
 C/Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
 C/Accession: A43848
 R/Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
 Infect. Immun. 60, 899-906, 1992
 A/Title: Binding of heparan sulfate to Staphylococcus aureus.
 A/Reference number: A43848; MUID:92176005; PMID:1541563
 A/Accession: A43848
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-9 <LIA>
 A/Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 29.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
 DB 3 TGW 5

RESULT 24
 A31571
 hypertrehalosemic/adipokinetic hormone - bollworm
 N/Alternate names: Hez-HrTH
 C/Species: Heliothis zea (bollworm, corn earworm, tomato fruitworm)
 C/Date: 30-Jun-1989 #sequence_revision 23-Mar-1995 #text_change 31-Oct-1997
 C/Accession: A31571
 R/Jaffe, H.; Raina, A.K.; Riley, C.T.; Fraser, B.A.; Bird, T.G.; Tseng, C.M.; Zhang, Y.S.
 Biochem. Biophys. Res. Commun. 155, 344-350, 1988
 A/Title: Isolation and primary structure of a neuropeptide hormone from Heliothis zea wit
 A/Reference number: A31571; MUID:88326324; PMID:3415690
 A/Accession: A31571
 A/Molecule type: protein
 A/Residues: 1-10 <JAF>
 C/Superfamily: adipokinetic hormone
 C/Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F/10/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 5e+03;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
 DB 3 TFWSSW 8

RESULT 25
 A61337
 caerulein - frog (Hyla caerulea)
 C/Species: Hyla caerulea
 C/Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C/Accession: A61337
 R/Anastasi, A.; Erspamer, V.; Endean, R.
 Arch. Biochem. Biophys. 125, 57-68, 1968
 A/Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the sh
 A/Reference number: A61337; MUID:68238534; PMID:5649531

A:Accession: A61337
A:Molecule type: Protein
A:Residues: 1-10 <ANA>
C:Comment: The last five amino acids and the carboxyl terminal amide group of this neuro
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid; se
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:4/Binding site: sulfate (Tyr) (covalent) #status experimental
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TAW 10
| |
5 TCW 7

RESULT 26
A53709
alpha-conotoxin ImI - cone shell (Conus imperialis)
N:Alternate names: alpha-CTX-ImI
C:Species: Conus imperialis (imperial cone)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A53709
R:McIntosh, J.M.; Yoshikami, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; Oliv
J. Biol. Chem. 269, 16733-16739, 1994
A:Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conotoxi
A:Reference number: A53709; MUID:94266889; PMID:8206995
A:Accession: A53709
A:Molecule type: protein
A:Residues: 1-12 <MCI>
A:Note: structure confirmed by chemical synthesis
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F:2-8,3-12/Disulfide bonds: #status experimental
F:12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 29.1%; Score 16; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 6.1e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
| |
7 RCW 10

RESULT 27
PC2369
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC2369
R:Matsumo, K.; Miyamoto, T.; Yamauchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanoo, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation i
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2369
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <MAS>

Query Match 29.1%; Score 16; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 6.6e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 TVKTAW 10
| |
5 TTENPW 10

RESULT 28
B19434
probable sex-specific protein 2 - Elaphe radiata
C:Species: Elaphe radiata
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1993
C:Accession: B19434
R:Epplen, J.T.; McCarrey, J.R.; Sutou, S.; Ohno, S.
Proc. Natl. Acad. Sci. U.S.A. 79, 3798-3802, 1982
A:Title: Base sequence of a cloned snake W-chromosome DNA fragment and identification of
A:Reference number: A19434; MUID:82247938; PMID:6954524
A:Accession: B19434
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <EPP>

Query Match 29.1%; Score 16; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 6.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FITTV 6
| | |
5 FIVIL 9

RESULT 29
PH1627
Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1627
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1627
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 29.1%; Score 16; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKT 8
| | | |
5 VTRET 10

RESULT 30
AKLQIM
locustamyoinhibiting peptide - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C:Accession: A60065
R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Regul. Pept. 36, 111-119, 1991
A:Title: Isolation, identification and synthesis of locustamyoinhibiting peptide
A:Reference number: A60065; MUID:92179466; PMID:1796179
A:Accession: A60065
A:Molecule type: protein
A:Residues: 1-9 <SCH>
C:Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and o
C:Superfamily: locustamyoinhibiting peptide
C:Keywords: amidated carboxyl end; hormone
F:9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 27.3%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 13

Db 1 AW 2
||

RESULT 31

C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A;Reference number: A57444; PMID:95403341; PMID:7673141
A;Accession: C57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
||
Db 1 AW 2

RESULT 32

D57444
neuropeptide Grb-AST B4 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: D57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A;Reference number: A57444; PMID:95403341; PMID:7673141
A;Accession: D57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
||
Db 1 AW 2

RESULT 33

A28924
fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 07-Feb-1997
C;Accession: A28924
R;Lacko, A.G.; Brox, L.W.; Gracy, R.W.; Horecker, B.L.
J. Biol. Chem. 245, 2140-2141, 1970
A;Title: The carboxyl-terminal structure of rabbit liver aldolase (aldolase B).
A;Reference number: A28924; PMID:70166720; PMID:5440846
A;Accession: A28924
A;Molecule type: protein
A;Residues: 1-9 <LAK>
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; per

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITT 5
||

Db 2 FLATT 6

RESULT 34

PT0634
T-cell receptor beta chain V-D-J region (121-2CL) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0634
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; PMID:91277601; PMID:1711558
A;Accession: PT0634
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-9 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 27.3%; Score 15; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 AW 10
||
Db 5 AW 6

RESULT 35

SPPGNK
neuromedin K - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 23-Aug-1996
C;Accession: A01560
R;Kangawa, K.; Minamino, N.; Fukuda, A.; Matsuo, H.
Biochem. Biophys. Res. Commun. 114, 533-540, 1983
A;Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.
A;Reference number: A01560; PMID:83282812; PMID:6576785
A;Accession: A01560
A;Molecule type: protein
A;Residues: 1-10 <KAN>
A;Note: the structure of the peptide was confirmed by synthesis
C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth muscle
C;Superfamily: neurokinin B precursor
C;Keywords: amidated carboxyl end; hormone; spinal cord
F;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 27.3%; Score 15; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FFI 3
||
Db 5 FFV 7

RESULT 36

S66248
processing enzyme, 33K - black gram (fragment)
C;Species: Vigna mungo (black gram)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S66248
R;Okamoto, T.; Minamikawa, T.
Eur. J. Biochem. 231, 300-305, 1995
A;Title: Purification of a processing enzyme (VmpB-1) that is involved in post-translational
A;Reference number: S66248; PMID:95361851; PMID:7635141
A;Accession: S66248
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <OKA>

Query Match 27.3%; Score 15; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 TAW 10
|||
Db 4 TRW 6

RESULT 37
A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C:Accession: A27617
R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A:Reference number: A34167
A:Accession: A27617
A:Molecule type: protein
A:Residues: 1-10 <BAU>
C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pentose

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PFI 3
|||
Db 4 FFV 6

RESULT 38
PN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PN0165
R:Fukaya, N.; Chow, L.P.; Sugiyama, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JPIB, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A:Reference number: PN0160
A:Accession: PN0165
A:Molecule type: protein
A:Residues: 1-10 <FUK>
A:Experimental source: strain M-1-1
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 PFI 3
|||
Db 4 FFV 6

RESULT 39
A35556
hypothetical protein (ODC region) - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C:Accession: A35556
R:Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosescu, J.; Almodovar, K.M.; Luk, G.D.
J. Biol. Chem. 265, 4884-4892, 1990
A:Title: Isolation and expression of a human ornithine decarboxylase gene.
A:Reference number: A35556; MUID:90202959; PMID:2318872
A:Accession: A35556
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <MOS>
A:Cross-references: GB:J05271

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PFI 3
|||
Db 4 FFV 6

RESULT 39
A35556
hypothetical protein (ODC region) - human
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 30-Sep-1993
C:Accession: A35556
R:Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosescu, J.; Almodovar, K.M.; Luk, G.D.
J. Biol. Chem. 265, 4884-4892, 1990
A:Title: Isolation and expression of a human ornithine decarboxylase gene.
A:Reference number: A35556; MUID:90202959; PMID:2318872
A:Accession: A35556
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <MOS>
A:Cross-references: GB:J05271

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 AW 10
|||
Db 7 AW 8

RESULT 40
TI3838
cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)
C:Species: mitochondrion Bipes biporus
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: TI3838
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826; PMID:9000757
A:Accession: TI3838
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71335; NID:gl753232; PID:gl753235; PIDN:AAB48271.1
C:Genetics:
A:Genome: mitochondrion
A>Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PFIT 4
|||
Db 7 FFST 10

RESULT 41
TI3976
cytochrome-c oxidase (EC 1.9.3.1) chain I - Cnemidophorus tigris mitochondrion (fragment)
C:Species: mitochondrion Cnemidophorus tigris
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: TI3976
R:Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.
Mol. Biol. Evol. 14, 91-104, 1997
A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
A:Reference number: Z17789; MUID:97153826; PMID:9000757
A:Accession: TI3976
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <MAC>
A:Cross-references: EMBL:U71332; NID:gl753236; PID:gl753239; PIDN:AAB48274.1
C:Genetics:
A:Genome: mitochondrion
A>Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.8e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PFIT 4
|||
Db 7 FFST 10

RESULT 42
TI7057
cytochrome-c oxidase (EC 1.9.3.1) chain I - Crotaphytus collaris mitochondrion (fragment)
C:Species: mitochondrion Crotaphytus collaris
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C:Accession: TI7057

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial genome

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17057

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U82681; NID:g3603108; PID:g3603111; PIDN:AAC62272.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 7.8e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FFIT 4

|||

Db 7 FFST 10

RESULT 43

T12303

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Diposaurus dorsalis mitochondrion (fragment)

C;Species: mitochondrion Diposaurus dorsalis

C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 22-Oct-1999

C;Accession: T12303

R;Schulte, J.A.; Macey, J.R.; Larson, A.; Papenfuss, T.J.

Mol. Phylogenet. Evol. 10, 367-376, 1998

A;Title: Molecular tests of phylogenetic taxonomies: A general procedure and example using

A;Reference number: Z17488; MUID:99162288; PMID:10051389

A;Accession: T12303

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <SCH>

A;Cross-references: EMBL:AF049857; NID:g4105726; PID:g4105729; PIDN:AAD02514.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 7.8e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FFIT 4

|||

Db 7 FFST 10

RESULT 44

T14019

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Eremitas grammica mitochondrion (fragment)

C;Species: mitochondrion Eremitas grammica

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000

C;Accession: T14019

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.

Mol. Biol. Evol. 14, 91-104, 1997

A;Title: Two novel gene orders and the role of light-strand replication in rearrangement

A;Reference number: Z17789; MUID:97153826; PMID:9000757

A;Accession: T14019

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U71331; NID:g1753240; PID:g1753243; PIDN:AAB48277.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 15; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 7.8e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FFIT 4

|||

Db 7 FFST 10

RESULT 45

T17060

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Gambelia wislizenii mitochondrion (fragment)

C;Species: mitochondrion Gambelia wislizenii

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999

C;Accession: T17060

R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997

A;Title: Evolutionary shifts in three major structural features of the mitochondrial genome

A;Reference number: Z18674; MUID:97315309; PMID:9169559

A;Accession: T17060

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U82682; NID:g3603120; PID:g3603123; PIDN:AAC62281.1

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match

27.3%; Score 15; DB 2; Length 10;

Best Local Similarity

75.0%; Pred. No. 7.8e+03;

Matches

3; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

Qy 1 FFIT 4

|||

Db 7 FFST 10

Search completed: August 30, 2004, 10:58:53

Job time : 4.00676 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 12.2297 Seconds
(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-9
Perfect score: 55
Sequence: 1 FFITVKTAW 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	54.5	13	10	US-09-991-225-19
2	30	54.5	13	10	US-09-991-225-38
3	30	54.5	13	12	US-10-369-405-19
4	30	54.5	13	12	US-10-369-405-38
5	27	49.1	13	14	US-10-174-105A-184
6	25	45.5	9	10	US-09-932-165-452
7	25	45.5	9	10	US-09-932-165-660
8	25	45.5	9	10	US-09-932-165-872
9	25	45.5	10	10	US-09-932-165-558
10	25	45.5	10	10	US-09-932-165-751
11	25	45.5	10	10	US-09-932-165-1369
12	25	45.5	10	10	US-09-932-165-1372
13	25	45.5	10	12	US-10-601-837-88
14	25	45.5	10	16	US-10-432-234A-31
15	25	45.5	10	16	US-10-432-234A-32

16	25	45.5	12	14	US-10-286-457-425	Sequence 425, App
17	24	43.6	8	14	US-10-224-999A-126	Sequence 126, App
18	24	43.6	9	14	US-10-224-999A-131	Sequence 131, App
19	24	43.6	9	14	US-10-224-999A-132	Sequence 132, App
20	24	43.6	10	14	US-10-224-999A-137	Sequence 137, App
21	24	43.6	10	14	US-10-224-999A-138	Sequence 138, App
22	24	43.6	10	14	US-10-224-999A-139	Sequence 139, App
23	24	43.6	11	14	US-10-224-999A-144	Sequence 144, App
24	24	43.6	11	14	US-10-224-999A-145	Sequence 145, App
25	24	43.6	11	14	US-10-224-999A-146	Sequence 146, App
26	24	43.6	11	14	US-10-224-999A-147	Sequence 147, App
27	24	43.6	12	14	US-10-224-999A-152	Sequence 152, App
28	24	43.6	12	14	US-10-224-999A-153	Sequence 153, App
29	24	43.6	12	14	US-10-224-999A-154	Sequence 154, App
30	24	43.6	12	14	US-10-224-999A-155	Sequence 155, App
31	24	43.6	12	14	US-10-224-999A-156	Sequence 156, App
32	24	43.6	12	16	US-10-203-969A-235	Sequence 235, App
33	24	43.6	12	16	US-10-203-969A-236	Sequence 236, App
34	24	43.6	12	16	US-10-203-969A-237	Sequence 237, App
35	24	43.6	12	16	US-10-203-969A-238	Sequence 238, App
36	24	43.6	12	16	US-10-203-969A-418	Sequence 418, App
37	24	43.6	12	16	US-10-203-969A-419	Sequence 419, App
38	24	43.6	12	16	US-10-203-969A-420	Sequence 420, App
39	24	43.6	12	16	US-10-642-553-102	Sequence 102, App
40	24	43.6	12	16	US-10-642-553-103	Sequence 103, App
41	24	43.6	12	16	US-10-642-553-104	Sequence 104, App
42	24	43.6	12	16	US-10-642-553-105	Sequence 105, App
43	24	43.6	12	16	US-10-642-553-275	Sequence 275, App
44	24	43.6	13	14	US-10-219-834-95	Sequence 95, Appl
45	24	43.6	13	14	US-10-224-999A-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-09-991-225-19
; Sequence 19, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY11, EXPRESSED HIS
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075.NP
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-991-225-19

Query Match 54.5% Score 30; DB 10; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qv 3 ITTVKTAW 10
;:::|
Db 4 VTSIRSAW 11

RESULT 2
US-09-991-225-38
; Sequence 38, Application US/09991225
; Publication No. US20030153063A1

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; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, EXPRESSED HI
; TITLE OF INVENTION: HEART AND VARIANTS THEREOF
; FILE REFERENCE: D0075A.CIP
; CURRENT APPLICATION NUMBER: US/09/991,225
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-225-38

Query Match          54.5%; Score 30; DB 10; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
   :|:::|
Db 4 VTSIRSAW 11

RESULT 3
US-10-369-405-19
; Sequence 19, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY11, AND VARIANTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0075A.CIP
; CURRENT APPLICATION NUMBER: US/10/369,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 13
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-369-405-19

Query Match          54.5%; Score 30; DB 12; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
   :|:::|
Db 4 VTSIRSAW 11

RESULT 4
US-10-369-405-38
; Sequence 38, Application US/10369405
; Publication No. US20030224400A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY11, AND VARIANTS
```

```
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: D0075A.CIP
; CURRENT APPLICATION NUMBER: US/10/369,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/249,613
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: U.S. 09/991,225
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/257,611
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: U.S. 60/305,818
; PRIOR FILING DATE: 2001-07-16
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-405-38

Query Match          54.5%; Score 30; DB 12; Length 13;
Best Local Similarity 37.5%; Pred. No. 1.3e+02;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
   :|:::|
Db 4 VTSIRSAW 11

RESULT 5
US-10-174-105A-184
; Sequence 184, Application US/10174105A
; Publication No. US20030068652A1
; GENERAL INFORMATION:
; APPLICANT: Cell Signaling Technology, Inc.
; APPLICANT: ZHANG, Hui
; APPLICANT: COMB, Michael J.
; APPLICANT: TAN, Yi
; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,
; TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
; FILE REFERENCE: CST-138 CIP3
; CURRENT APPLICATION NUMBER: US/10/174,105A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 09/148,712
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/535,364
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 193
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 184
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: PHOSPHORYLATION; threonine at position 5 is phosphorylated
US-10-174-105A-184

Query Match          49.1%; Score 27; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
   :|:::|
Db 3 LATVKSRL 10

RESULT 6
US-09-932-165-452
; Sequence 452, Application US/09932165
```


; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 452
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-452

Query Match 45.5%; Score 25; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
|||:|
Db 3 PFFTNIK 9

RESULT 7
US-09-932-165-660
; Sequence 660, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 660
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-660

Query Match 45.5%; Score 25; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
|||:|
Db 3 PFFTNIK 9

RESULT 8
US-09-932-165-872
; Sequence 872, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 872
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-872

Query Match 45.5%; Score 25; DB 10; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFITTVK 7
|||:|
Db 1 PFFTNIK 7

RESULT 9
US-09-932-165-558
; Sequence 558, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatF2E11 USEFUL IN TREATMENT AND
; FILE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 558
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-558

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-558

Query Match          45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFTTVK 7
   ||| :|
Db 4 FFTNIK 10

RESULT 10
US-09-932-165-751
; Sequence 751, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARRIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-P2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 751
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-751

Query Match          45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFTTVK 7
   ||| :|
Db 4 FFTNIK 10

RESULT 11
US-09-932-165-1369
; Sequence 1369, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARRIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-P2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1369
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1369

Query Match          45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFTTVK 7
   ||| :|
Db 4 FFTNIK 10

RESULT 12
US-09-932-165-1372
; Sequence 1372, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARRIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-P2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1372
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1372

Query Match          45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFTTVK 7
   ||| :|
Db 1 FFTNIK 7

RESULT 13
US-10-601-837-88
; Sequence 88, Application US/10601837
; Publication No. US2004005309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
```

```
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1369
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1369

Query Match          45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFTTVK 7
   ||| :|
Db 2 FFTNIK 8

RESULT 12
US-09-932-165-1372
; Sequence 1372, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARRIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND Cat-P2E11 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1372
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1372

Query Match          45.5%; Score 25; DB 10; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FFTTVK 7
   ||| :|
Db 1 FFTNIK 7

RESULT 13
US-10-601-837-88
; Sequence 88, Application US/10601837
; Publication No. US2004005309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
```

```
; APPLICANT: Moyses, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidn
; TITLE OF INVENTION: Response
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601.837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Ratus No. US20040053309Alvegicus
US-10-601-837-88

Query Match          45.5%; Score 25; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FITTVK 7
Db 3 FITTVQ 8

RESULT 14
US-10-432-234A-31
; Sequence 31, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:
; APPLICANT: Biota Scientific Management Pty Ltd
; TITLE OF INVENTION: A method of expression and agents identified thereby
; FILE REFERENCE: 12084720/TDO
; CURRENT APPLICATION NUMBER: US/10/432.234A
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/252767
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-432-234A-31

Query Match          45.5%; Score 25; DB 16; Length 10;
Best Local Similarity 22.2%; Pred. No. 7.9e+02;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FITTVK 7
Db 2 YLSALRTGW 10

RESULT 15
US-10-432-234A-32
; Sequence 32, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:
; APPLICANT: Biota Scientific Management Pty Ltd
; TITLE OF INVENTION: A method of expression and agents identified thereby
; FILE REFERENCE: 12084720/TDO
; CURRENT APPLICATION NUMBER: US/10/432.234A
; CURRENT FILING DATE: 2003-05-22
; PRIOR APPLICATION NUMBER: US 60/252767
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 574
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 10
; TYPE: PRT
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```
; ORGANISM: respiratory syncytial virus
US-10-432-234A-32

Query Match          45.5%; Score 25; DB 16; Length 10;
Best Local Similarity 22.2%; Pred. No. 7.9e+02;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FITTVK 7
Db 1 YLSALRTGW 9

RESULT 16
US-10-286-457-425
; Sequence 425, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286.457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 425
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-425

Query Match          45.5%; Score 25; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TVKTAW 10
Db 1 TVKAGW 6

RESULT 17
US-10-224-999A-126
; Sequence 126, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224.999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-126

Query Match          43.6%; Score 24; DB 14; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
Db 1 ITTVKTA 9
```

Db 1 LTTVPTA 7

RESULT 18

US-10-224-999A-131

; Sequence 131, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 131

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-131

Query Match 43.6%; Score 24; DB 14; Length 9;

Best Local Similarity 71.4%; Pred. No. 1.2e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9

:|||

Db 2 LTTVPTA 8

RESULT 19

US-10-224-999A-132

; Sequence 132, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 132

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-132

Query Match 43.6%; Score 24; DB 14; Length 9;

Best Local Similarity 71.4%; Pred. No. 1.2e+06;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9

:|||

Db 1 LTTVPTA 7

RESULT 20

US-10-224-999A-137

; Sequence 137, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 137

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-137

Query Match 43.6%; Score 24; DB 14; Length 10;

Best Local Similarity 71.4%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9

:|||

Db 2 LTTVPTA 8

RESULT 21

US-10-224-999A-138

; Sequence 138, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 138

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-138

Query Match 43.6%; Score 24; DB 14; Length 10;

Best Local Similarity 71.4%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9

:|||

Db 2 LTTVPTA 8

RESULT 22

US-10-224-999A-139

; Sequence 139, Application US/10224999A

; Publication No. US20030171318A1

; GENERAL INFORMATION:

; APPLICANT: Myriad Genetics, Inc.

; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton

; APPLICANT: Hobden, Adrian

; TITLE OF INVENTION: Composition and Method for Treating Viral Infection

; FILE REFERENCE: 5004.01

; CURRENT APPLICATION NUMBER: US/10/224,999A

; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: US 60/313,695

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 139

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Hepatitis B virus

US-10-224-999A-139

Query Match 43.6%; Score 24; DB 14; Length 10;

Best Local Similarity 71.4%; Pred. No. 1.2e+03;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9

:|||

Db 2 LTTVPTA 8

; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-139

Query Match 43.6%; Score 24; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
Db 1 LTTVPTA 7

RESULT 23
US-10-224-999A-144
; Sequence 144, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 144
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-144

Query Match 43.6%; Score 24; DB 14; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
Db 4 LTTVPTA 10

RESULT 24
US-10-224-999A-145
; Sequence 145, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-145

Query Match 43.6%; Score 24; DB 14; Length 11;

Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
Db 3 LTTVPTA 9

RESULT 25
US-10-224-999A-146
; Sequence 146, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-146

Query Match 43.6%; Score 24; DB 14; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
Db 2 LTTVPTA 8

RESULT 26
US-10-224-999A-147
; Sequence 147, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-147

Query Match 43.6%; Score 24; DB 14; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 ITTVKTA 9
Db 1 LTTVPTA 7

RESULT 27

```
US-10-224-999A-152
; Sequence 152, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-152
```

```
Query Match 43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ITTVKTA 9
:|||||
Db 5 LTTVPTA 11
```

```
RESULT 28
US-10-224-999A-153
; Sequence 153, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 153
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-153
```

```
Query Match 43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ITTVKTA 9
:|||||
Db 4 LTTVPTA 10
```

```
RESULT 29
US-10-224-999A-154
; Sequence 154, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
```

```
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-154
```

```
Query Match 43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ITTVKTA 9
:|||||
Db 3 LTTVPTA 9
```

```
RESULT 30
US-10-224-999A-155
; Sequence 155, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-155
```

```
Query Match 43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ITTVKTA 9
:|||||
Db 2 LTTVPTA 8
```

```
RESULT 31
US-10-224-999A-156
; Sequence 156, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 12
```

```
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-156

Query Match      43.6%; Score 24; DB 14; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ITTVKTA 9
   |::|||
Db 1 LTTVPTA 7

RESULT 32
US-10-203-969A-235
; Sequence 235, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Sijlstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/10/203,969A
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 235
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-235

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
   |::|||
Db 4 FCISINTW 12

RESULT 33
US-10-203-969A-236
; Sequence 236, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Sijlstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/10/203,969A
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 236
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(12)
US-10-203-969A-236

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
   |::|||
Db 2 FCISINTW 10

RESULT 35
US-10-203-969A-238
; Sequence 238, Application US/10203969A
; Publication No. US20040110224A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C.
; APPLICANT: Sijlstra, Jelle W.
; TITLE OF INVENTION: Segment synthesis
; FILE REFERENCE: P50200US00
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/10/203,969A
; PRIOR FILING DATE: 2000-02-16
; PRIOR APPLICATION NUMBER: EP 00200536.1
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/NL01/00131
; PRIOR FILING DATE: 2001-02-16
```

; NUMBER OF SEQ ID NOS: 660
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 238
; LENGTH: 12

; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 12-mer peptide
; OTHER INFORMATION: derived from hFSH

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)..(12)

US-10-203-969A-238

Query Match 43.6%; Score 24; DB 16; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10

Db 1 FCISINTTW 9

RESULT 36

US-10-203-969A-418

; Sequence 418, Application US/10203969A

; Publication No. US20040110224A1

; GENERAL INFORMATION:

; APPLICANT: Puijk, Wouter C.

; APPLICANT: Dijk van, Evert

; APPLICANT: Slootstra, Jelle W.

; TITLE OF INVENTION: Segment synthesis

; FILE REFERENCE: P50200US00

; CURRENT APPLICATION NUMBER: US/10/203,969A

; CURRENT FILING DATE: 2003-07-07

; PRIOR APPLICATION NUMBER: EP 00200536.1

; PRIOR FILING DATE: 2000-02-16

; PRIOR APPLICATION NUMBER: PCT/NL01/00131

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 660

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 418

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: 11-mer peptide

; OTHER INFORMATION: derived from hFSH with an additional C- or N-

; OTHER INFORMATION: terminal cysteine

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)..(12)

US-10-203-969A-418

Query Match 43.6%; Score 24; DB 16; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10

Db 3 FCISINTTW 11

RESULT 37

US-10-203-969A-419

; Sequence 419, Application US/10203969A

; Publication No. US20040110224A1

; GENERAL INFORMATION:

; APPLICANT: Puijk, Wouter C.

; APPLICANT: Dijk van, Evert

; APPLICANT: Slootstra, Jelle W.

; TITLE OF INVENTION: Segment synthesis

; FILE REFERENCE: P50200US00

; CURRENT APPLICATION NUMBER: US/10/203,969A

; CURRENT FILING DATE: 2003-07-07

; PRIOR APPLICATION NUMBER: EP 00200536.1

; PRIOR FILING DATE: 2000-02-16

; PRIOR APPLICATION NUMBER: PCT/NL01/00131

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 660

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 419

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: 11-mer peptide

; OTHER INFORMATION: derived from hFSH with an additional C- or N-

; OTHER INFORMATION: terminal cysteine

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)..(12)

US-10-203-969A-419

Query Match 43.6%; Score 24; DB 16; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10

Db 3 FCISINTTW 11

RESULT 38

US-10-203-969A-420

; Sequence 420, Application US/10203969A

; Publication No. US20040110224A1

; GENERAL INFORMATION:

; APPLICANT: Puijk, Wouter C.

; APPLICANT: Dijk van, Evert

; APPLICANT: Slootstra, Jelle W.

; TITLE OF INVENTION: Segment synthesis

; FILE REFERENCE: P50200US00

; CURRENT APPLICATION NUMBER: US/10/203,969A

; CURRENT FILING DATE: 2003-07-07

; PRIOR APPLICATION NUMBER: EP 00200536.1

; PRIOR FILING DATE: 2000-02-16

; PRIOR APPLICATION NUMBER: PCT/NL01/00131

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 660

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 420

; LENGTH: 12

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: 11-mer peptide

; OTHER INFORMATION: derived from hFSH with an additional C- or N-

; OTHER INFORMATION: terminal cysteine

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)..(12)

US-10-203-969A-420

Query Match 43.6%; Score 24; DB 16; Length 12;

Best Local Similarity 33.3%; Pred. No. 1.4e+03;

Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10

Db 1 FCISINTTW 9

RESULT 39

US-10-642-553-102

; Sequence 102, Application US/10642553


```
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-102

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 FITVKTAW 10
Db      4 FCISINTW 12

RESULT 40
US-10-642-553-103
; Sequence 103, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-103

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 FITVKTAW 10
Db      3 FCISINTW 11

RESULT 41
US-10-642-553-104
; Sequence 104, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
```

```
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 104
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-104

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 FITVKTAW 10
Db      2 FCISINTW 10

RESULT 42
US-10-642-553-105
; Sequence 105, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-642-553-105

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      2 FITVKTAW 10
Db      1 FCISINTW 9

RESULT 43
US-10-642-553-275
; Sequence 275, Application US/10642553
; Publication No. US20040114780A1
; GENERAL INFORMATION:
; APPLICANT: Puijk, Wouter C
; APPLICANT: Evert, van Dijk
; APPLICANT: Jelle, Slootstra W
; TITLE OF INVENTION: PIXEL ARRAYS
; FILE REFERENCE: 2183-6064
; CURRENT APPLICATION NUMBER: US/10/642,553
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/NL02/00097
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: EP 01200551.8
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 386
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 275
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fragment of hFSH with Cys attached to the C or N terminal
US-10-642-553-275

Query Match      43.6%; Score 24; DB 16; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 FFTVKTAW 10
      ||::||
Db      1 FCISINTW 9

RESULT 44
US-10-219-834-95
; Sequence 95, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219,834
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313,658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-95

Query Match      43.6%; Score 24; DB 14; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 FFTVKTAW 10
      ||::||
Db      2 FFGSFRKQW 11

RESULT 45
US-10-224-999A-161
; Sequence 161, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-224-999A-161

Query Match      43.6%; Score 24; DB 14; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 LTTVXTA 9
      :|||
Db      6 LTTVPTA 12

Search completed: August 30, 2004, 11:05:01
Job time : 13.2297 secs
```


Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTVKTAW 10
| | | | |
Db 8 TTVKAAW 14

RESULT 2

US-08-188-374-7
; Sequence 7, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aitken F., Jacqueline
; APPLICANT: Apostol, Izidor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Meth
; FILE REFERENCE: BXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; CURRENT FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide from
; OTHER INFORMATION: horse, donkey, kulan, zebra or gundi
US-08-188-374-7

Query Match 52.7%; Score 29; DB 3; Length 14;
Best Local Similarity 71.4%; Pred. No. 55;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TTVKTAW 10
| | | | |
Db 8 TTVKAAW 14

RESULT 3

US-08-637-759B-97
; Sequence 97, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-97

Query Match 41.8%; Score 23; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TTVKTAW 10
| | | | |
Db 1 TTVNTHW 6

RESULT 4

US-08-871-355A-97
; Sequence 97, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-97

Query Match 41.8%; Score 23; DB 3; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 TTVKTAW 10

IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-5
Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 7 KTAW 10
DB 5 KTSW 8
RESULT 8
US-08-467-472C-6
Sequence 6, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK

STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LXR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:

PUBLICATION DATE: 40.0%; Score 22; DB 3; Length 8;
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-08-467-472C-6
Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 7 KTAW 10
Db 5 KTSW 8

RESULT 9
US-09-384-061-5
Sequence 5, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: ENANTIOMER
LOCATION: -4
IDENTIFICATION METHOD: amino acid analysis
IDENTIFICATION METHOD: and
IDENTIFICATION METHOD: mass spectrometry
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-5

Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KTAW 10
Db 5 KTSW 8

RESULT 10
US-09-384-061-6
; Sequence 6, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HADDT HAPFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: ENANTIOMER
; LOCATION: -4
; IDENTIFICATION METHOD: amino acid analysis
; IDENTIFICATION METHOD: and
; IDENTIFICATION METHOD: mass spectrometry
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:

; FILING DATE:
; PUBLICATION RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION RESIDUES IN SEQ ID NO: 6: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; PUBLICATION RESIDUES IN SEQ ID NO: 6: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-6
Query Match 40.0%; Score 22; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 KTAW 10
Db 5 KTSW 8
RESULT 11
US-09-852-870A-5
; Sequence 5, Application US/09852870A
; Patent No. 6673789
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osabay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-5
Query Match 40.0%; Score 22; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 KTAW 10
||:|

Db 5 KTSW 8

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
; NAME/KEY: SITE
; LOCATION: (1)..(8)
; OTHER INFORMATION: Xaa= D-Phe, D-beta-Nal, or Phe
US-09-852-870A-6

Query Match 40.0%; Score 22; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTW 10
Db 7 KTSW 10

RESULT 14

US-08-727-688-24
; Sequence 24, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5919638e
US-08-727-688-24

Query Match 40.0%; Score 22; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 7.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 VKTAW 10
Db 2 METAW 6

RESULT 12

US-08-704-655-20
; Sequence 20, Application US/08704655
; Patent No. 5869453
; GENERAL INFORMATION:
; APPLICANT: Moss, Denis J.
; APPLICANT: Burrows, Scott R.
; APPLICANT: Khanna, Rajiv
; APPLICANT: Kerr, Veberly M.
; APPLICANT: Burrows, Jacqueline M.
; APPLICANT: Subrier, Andreas
; TITLE OF INVENTION: Cytotoxic T Cell Epitopes
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,655
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU95/00140
; FILING DATE: 16-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: FBR002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (712) 789-2679
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-704-655-20

Query Match 40.0%; Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
Db 3 ITPYKPTW 10

RESULT 13

US-09-852-870A-6
; Sequence 6, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24

RESULT 15
US-09-113-977C-9
; Sequence 9, Application US/09113977C
; Patent No. 6277824
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; FILE REFERENCE: 100086.403
; CURRENT APPLICATION NUMBER: US/09/113,977C
; CURRENT FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; NAME/KEY: MOD RES
; LOCATION: (1)...(1)
; OTHER INFORMATION: Residue may be native or modified
; NAME/KEY: MOD RES
; LOCATION: (11)...(11)
; OTHER INFORMATION: Residue may be native or modified
US-09-113-977C-9

Query Match 40.0%; Score 22; DB 3; Length 11;
Best Local Similarity 44.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
||| :||
Db 2 FIIRERTGW 10

RESULT 16
US-09-351-048A-9
; Sequence 9, Application US/09351048A
; Patent No. 6472368
; GENERAL INFORMATION:
; APPLICANT: Doherty, Patrick
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE
; FILE REFERENCE: 100086.403C1
; CURRENT APPLICATION NUMBER: US/09/351,048A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
US-09-351-048A-9

Query Match 40.0%; Score 22; DB 4; Length 11;
Best Local Similarity 44.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 FITTVKTAW 10
||| :||
Db 2 FIIRERTGW 10

RESULT 17
US-09-069-827A-42
; Sequence 42, Application US/09069827A
; Patent No. 6617114
; GENERAL INFORMATION:
; APPLICANT: FOWLKES, Dana M
; KAY, Brian K
; FRELINGER, Jeffrey A
; HYDE-DERUYSCHE, Robin P
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
; COMPLEMENTARY COMBINATORIAL LIBRARIES
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEWMARK, P.L.L.C.
; STREET: 624 Ninth Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-Apr-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-09-069-827A-42

Query Match 40.0%; Score 22; DB 4; Length 11;
Best Local Similarity 37.5%; Pred. No. 7.2e+02;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
:|:|:
Db 2 VFTTKVLW 9

RESULT 18
US-09-832-161-27
; Sequence 27, Application US/09832161
; Patent No. 6656713
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinnon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris

; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832.161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-27

Query Match 40.0%; Score 22; DB 4; Length 12;
Best Local Similarity 37.5%; Pred. No. 7.8e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 ITTVKTA 10
| | : : |
Db 4 IETIESNW 11

RESULT 19
5496924-54
; Patent No. 5496924
; APPLICANT: HABERMANN, PAUL; WENGENMAYER, FRIEDRICH
; TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN
; INTERLEUKIN-2 FRAGMENT BALLAST PORTION
; NUMBER OF SEQUENCES: 56
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,545
; FILING DATE: 28-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 377,313
; FILING DATE: 10-JUL-1989
; APPLICATION NUMBER: 934,910
; FILING DATE: 25-NOV-1986
; APPLICATION NUMBER: 943,804
; FILING DATE: 19-DEC-1986
; SEQ ID NO: 54
; LENGTH: 13
5496924-54

Query Match 40.0%; Score 22; DB 6; Length 13;
Best Local Similarity 55.6%; Pred. No. 8.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 FFITVTKTA 9
| | : : |
Db 2 FMITVSLA 10

RESULT 20
5496924-48
; Patent No. 5496924
; APPLICANT: HABERMANN, PAUL; WENGENMAYER, FRIEDRICH
; TITLE OF INVENTION: FUSION PROTEIN COMPRISING AN
; INTERLEUKIN-2 FRAGMENT BALLAST PORTION
; NUMBER OF SEQUENCES: 56
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,545
; FILING DATE: 28-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 377,313
; FILING DATE: 10-JUL-1989
; APPLICATION NUMBER: 934,910
; FILING DATE: 25-NOV-1986
; APPLICATION NUMBER: 943,804
; FILING DATE: 19-DEC-1986
; SEQ ID NO: 48

; LENGTH: 14
5496924-48

Query Match 40.0%; Score 22; DB 6; Length 14;
Best Local Similarity 55.6%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 FFITVTKTA 9
| | : : |
Db 3 FMITVSLA 11

RESULT 21
US-08-233-558-20
; Sequence 20, Application US/08233558
; Patent No. 5480870
; GENERAL INFORMATION:
; APPLICANT: Keri, Gyorgy
; APPLICANT: Mezo, Imre
; APPLICANT: Horvath, Aniko
; APPLICANT: Vadasz, Zsolt
; APPLICANT: Teplan, Istvan
; APPLICANT: Balogh, Agnes
; APPLICANT: Csuka, Orsolya
; APPLICANT: Bokonyi, Gyongyi
; APPLICANT: Szoke, Balazs
; APPLICANT: Horvath, Judit
; TITLE OF INVENTION: No. 5480870el Tumour Growth-Inhibiting
; TITLE OF INVENTION: Somatostatin Analogues, Pharmaceutical Compositions
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauf
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 360 Kb storage
; COMPUTER: IBM AT-compatible, 80286 processor
; OPERATING SYSTEM: MS-DOS version 5.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA: US/08/233,558
; APPLICATION NUMBER: US/08/233,558
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/772,808
; FILING DATE: 08-OCT-1991
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-233-558-20

Query Match 38.2%; Score 21; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 KTAW 10
| | : : |
Db 5 KTCW 8

RESULT 22
US-08-405-647B-15
; Sequence 15, Application US/08405647B
; Patent No. 6124262
; GENERAL INFORMATION:
; APPLICANT: Sherman, Irwin W.

```
; APPLICANT: Crandall, Ian E.
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Thevenin, Bernard Jean-Marie
; TITLE OF INVENTION: Compositions and Methods for Reducing
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,647B
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 02307E-068700US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-405-647B-15

Query Match 38.2%; Score 21; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITVKT 8
Db 1 FVKRVKT 7

RESULT 23
US-09-074-658-52
; Sequence 52, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quifun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
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; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-658-52

Query Match 38.2%; Score 21; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 ITTVKT 8
Db 1 MSTVKT 6

RESULT 24
US-08-985-499-15
; Sequence 15, Application US/08985499
; Patent No. 6191103
; GENERAL INFORMATION:
; APPLICANT: Shohet, Stephen B.
; APPLICANT: Sherman, Irwin
; APPLICANT: von Andrian, Ulrich
; TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
; Molecule Type: Mammal
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,499
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymal, Laurence J.
; REGISTRATION NUMBER: 35,551
; REFERENCE/DOCKET NUMBER: 02307E-084500US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-985-499-15

Query Match 38.2%; Score 21; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 FITTVKT 8
| : |||
Db 1 FVKEVKT 7

RESULT 25
PCT-US96-03180-15
; Sequence 15, Application PC/TUS9603180
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University
; APPLICANT: of California
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
; TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90012-2628
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/03180
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Berliner, Robert
; REGISTRATION NUMBER: 20,121
; REFERENCE/DOCKET NUMBER: 5555-370
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-03180-15

Query Match 38.2%; Score 21; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FITTVKT 8
| : |||
Db 1 FVKEVKT 7

RESULT 26
5514646-27
; Patent No. 5514646
; APPLICANT: CHANCE, RONALD E.; DIMARCHI, RICHARD D.; FRANK,
; BRUCE H.; SHIELDS, JAMES E.
; TITLE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION
; 29 OF THE B CHAIN
; NUMBER OF SEQUENCES: 52
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/57,201
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 686,632
; FILING DATE: 17-APR-1991
; APPLICATION NUMBER: 388,201
; FILING DATE: 04-AUG-1989
; APPLICATION NUMBER: 308,352
; FILING DATE: 09-FEB-1989
; SEQ ID NO: 27;

; LENGTH: 8
5514646-27

Query Match 38.2%; Score 21; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FFYTT 5
| : |||
Db 2 FFYTT 6

RESULT 27
US-08-425-238-6
; Sequence 6, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-425-238-6

Query Match 38.2%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
| : |||
Db 4 ETAW 7

RESULT 28
US-08-425-238-10
; Sequence 10, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Campbell and Flores
;; STREET: 4370 La Jolla Village Drive, Suite 700
;; CITY: San Diego
;; STATE: California
;; COUNTRY: USA
;; ZIP: 92122
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/425,238
;; FILING DATE:
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/158,001
;; FILING DATE: 24-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LA 9775
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 1
;; OTHER INFORMATION: /note= "Xaa = an amino acid capable
;; OTHER INFORMATION: of forming a disulfide bond."
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: 9
;; OTHER INFORMATION: /note= "Xaa = an amino acid capable
;; OTHER INFORMATION: of forming a disulfide bond."
US-08-425-238-10

Query Match 38.2%; Score 21; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 4 ETAW 7

RESULT 29
US-08-717-169-18
; Sequence 18, Application US/08/717169
; Patent No. 5922676
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruostantti, Erkki
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronectin
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/717,169
;; FILING DATE: 20-SEP-1996
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Campbell, Cathryn A.
;; REGISTRATION NUMBER: 31,815
;; REFERENCE/DOCKET NUMBER: P-LJ 2017
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (619) 535-9001
;; TELEFAX: (619) 535-8949
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-717-169-18

Query Match 38.2%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 4 ETAW 7

RESULT 30
US-08-867-941-52
; Sequence 52, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loomsore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Quijun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-867-941-52

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;
; Query Match 38.2%; Score 21; DB 2; Length 9;
; Best Local Similarity 66.7%; Pred. No. 3e+05; Indels 0; Gaps 0;
; Matches 4; Conservative 2; Mismatches 0;
;
Qy 3 ITTVKT 8
Db 1 MSTVKT 6

;
; RESULT 31
; US-08-286-861-12
; Sequence 12, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NO. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
;
US-08-286-861-12

;
; Query Match 38.2%; Score 21; DB 2; Length 9;
; Best Local Similarity 75.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
; Matches 3; Conservative 1; Mismatches 0;
;
Qy 7 KTAW 10
Db 4 ETAW 7

;
; RESULT 32
; US-09-424-656-13
; Sequence 13, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; ENHANCED TRANSESECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
;
US-09-424-656-13

;
; Query Match 38.2%; Score 21; DB 4; Length 9;
; Best Local Similarity 75.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
; Matches 3; Conservative 1; Mismatches 0;
;
Qy 7 KTAW 10
Db 4 ETAW 7

;
; RESULT 33
; US-09-228-901A-18
; Sequence 18, Application US/09228901A
; Patent No. 6475488
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
; Ameliorating Cancer by Using Superfibronectin
; FILE REFERENCE: P-TX 3416
; CURRENT APPLICATION NUMBER: US/09/228,901A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 08/717,169
; PRIOR FILING DATE: 1996-09-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-228-901A-18

;
; Query Match 38.2%; Score 21; DB 4; Length 9;
; Best Local Similarity 75.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
; Matches 3; Conservative 1; Mismatches 0;
;
Qy 7 KTAW 10
Db 4 ETAW 7

;
; RESULT 34
; US-09-490-702B-89
; Sequence 89, Application US/09490702B
; Patent No. 6560542
; GENERAL INFORMATION:
; APPLICANT: Mandell, Arnold
; APPLICANT: Seitz, Karen
; APPLICANT: Shlesinger, Michael
; TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation of th
; FILE REFERENCE: 01561-0002-00US00
; CURRENT APPLICATION NUMBER: US/09/490,702B
; CURRENT FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: synthetic
US-09-490-702B-89

Query Match      38.2%; Score 21; DB 4; Length 10;
Best Local Similarity 25.0%; Pred. No. 9.8e+02;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 ITTVKTAW 10
   :|:|:|
Db 1 VOTISSRW 8

RESULT 35
US-09-424-656-11
; Sequence 11, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-11

Query Match      38.2%; Score 21; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
   :|:|:|
Db 6 ETAW 9

RESULT 36
US-09-424-656-12
; Sequence 12, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-424-656-12

Query Match      38.2%; Score 21; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
   :|:|:|
Db 6 ETAW 9

RESULT 37
US-09-424-656-12
; Sequence 12, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT: SPRINGER, TIMOTHY A.; STAUNTON, DONALD E.;
; DUSTIN, MICHAEL L.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
; ICAM-2
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/384,814
; FILING DATE: 06-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 89,3075
; FILING DATE: 12-JUL-1995
; APPLICATION NUMBER: 89,307
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 454,294
; FILING DATE: 22-DEC-1989
; APPLICATION NUMBER: 45,963
; FILING DATE: 04-MAY-1987
; APPLICATION NUMBER: 115,798
; FILING DATE: 02-NOV-1987
; APPLICATION NUMBER: 155,943
; FILING DATE: 16-FEB-1988
; APPLICATION NUMBER: 189,815
; FILING DATE: 03-MAY-1988
; APPLICATION NUMBER: 250,446
; FILING DATE: 28-SEP-1988
; SEQ ID NO: 16:
; LENGTH: 12
5489533-16

Query Match      38.2%; Score 21; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 VKTAW 10
   :|:|:|
Db 6 VRAAW 10

RESULT 38
US-09-424-656-12
; Sequence 12, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT: SPRINGER, TIMOTHY A.; STAUNTON, DONALD E.;
; DUSTIN, MICHAEL L.
; TITLE OF INVENTION: PURIFIED ICAM-2 AND FRAGMENT THEREOF
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,613
; FILING DATE: 10-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 89,307
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;
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 454,294
; FILING DATE: 22-DEC-1989
; APPLICATION NUMBER: 45,963
; FILING DATE: 04-MAY-1987
; APPLICATION NUMBER: 115,798
; FILING DATE: 02-NOV-1987
; APPLICATION NUMBER: 155,943
; FILING DATE: 16-FEB-1988
; APPLICATION NUMBER: 189,815
; FILING DATE: 03-MAY-1988
; APPLICATION NUMBER: 250,446
; FILING DATE: 28-SEP-1988
; SEQ ID NO:16:
; LENGTH: 12
5512660-16

Query Match 38.2%; Score 21; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KTAW 10
: |||
Db 6 VRAAW 10

RESULT 39
US-08-425-238-3
; Sequence 3, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-425-238-3
Query Match 38.2%; Score 21; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 KTAW 10
: |||
Db 6 VRAAW 10

RESULT 40
US-08-425-238-11
; Sequence 11, Application US/08425238
; Patent No. 5627263
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 3
; OTHER INFORMATION: /note= "Xaa = an amino acid capable
; OTHER INFORMATION: of forming a disulfide bond."
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 11
; OTHER INFORMATION: /note= "Xaa = an amino acid capable
; OTHER INFORMATION: of forming a disulfide bond."
US-08-425-238-11

Query Match 38.2%; Score 21; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KTAW 10
: |||
Db 6 ETAW 9

RESULT 41
US-08-701-124-35
; Sequence 35, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.

; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-35

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 6 ETAW 9

RESULT 42
US-08-286-861-6
; Sequence 6, Application US/08286861
; Patent No. 5981478
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,861
; FILING DATE: 04-AUG-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9992
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-286-861-6

Query Match 38.2%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 6 ETAW 9

RESULT 43
US-09-130-225-35
; Sequence 35, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,225
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-130-225-35

Query Match 38.2%; Score 21; DB 3; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KTAW 10
Db 6 ETAW 9

RESULT 44
US-09-177-249-199
; Sequence 199, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramon
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.

```

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-199

```

```

Query Match      38.2%; Score 21; DB 3; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      7 KTAW 10
DB      1 KTCW 4

```

```

RESULT 45
US-09-406-781-63
; Sequence 63, Application US/09406781
; Patent No. 6306663
; GENERAL INFORMATION:
; APPLICANT: Kenten, John
; APPLICANT: Roberts, Steven
; TITLE OF INVENTION: CONTROLLING PROTEIN LEVELS IN EUKARYOTIC ORGANISMS
; FILE REFERENCE: 2757-3
; CURRENT APPLICATION NUMBER: US/09/406,781
; CURRENT FILING DATE: 1999-09-28
; EARLIER APPLICATION NUMBER: 60/119,851
; EARLIER FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: binding peptide
US-09-406-781-63

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Query Match      38.2%; Score 21; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY      7 KTAW 10
DB      6 ETAW 9

```

Search completed: August 30, 2004, 10:57:20
Job time : 5.9527 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 309.892 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-44

Perfect score: 1083

Sequence: 1 MKVLLAAALAGSVFFLLLP.....VLIADCGKIEKPFALAKE 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	83	7.7	14	6	Abp74769 Proteome
2	71	6.6	11	3	Aay69925 Human cyc
3	63	5.8	10	3	Aay69947 Human cyc
4	63	5.8	10	6	AbR84352 Human cyp
5	63	5.8	11	3	Aay69926 Human cyp
6	60	5.5	11	3	Aay69924 Human cyp
7	58	5.4	9	3	Aay69928 Human cyp
8	58	5.4	10	3	Aay69930 Human cyp
9	57	5.3	11	3	Aay69944 Human cyp
10	55	5.1	10	3	Aay69929 Human cyp
11	55	5.1	11	3	Aay69943 Human cyp
12	54	5.0	14	5	Abg67616 Human ADP
13	54	5.0	14	6	Ada23735 Alzheimer
14	53	4.9	10	3	Aay69949 Human cyp
15	52	4.8	10	3	Aay69945 Human cyp
16	51	4.7	9	3	Aay69923 Human cyp
17	51	4.7	11	3	Aay69955 Human cyp
18	50	4.6	9	3	Aay69922 Human cyp
19	50	4.6	9	3	Aay69927 Human cyp
20	50	4.6	9	4	Aab46931 Human cyp
21	50	4.6	9	4	Aag68089 Antitumou
22	50	4.6	9	5	Abg79076 Human cyp
23	50	4.6	9	6	AbR84374 Human cyp
24	50	4.6	9	7	Adc17702 Cyclophil
25	50	4.6	10	3	Aay69939 Human cyp

26	50	4.6	11	3	AAY69935	Aay69935 Human cyc
27	50	4.6	11	3	AAY69938	Aay69938 Human cyc
28	49	4.5	9	3	AAY69921	Aay69921 Human cyc
29	49	4.5	9	4	AAB46930	Aab46930 Human cyc
30	49	4.5	9	4	AAG68088	Aag68088 Antitumou
31	49	4.5	9	5	ABG79075	Abg79075 Human cyp
32	49	4.5	9	6	ABR84373	AbR84373 Human cyp
33	49	4.5	9	7	ADC17701	Adc17701 Cyclophil
34	48	4.4	8	3	AAY69950	Aay69950 Human cyc
35	48	4.4	14	2	AAR72947	Aar72947 E. coli p
36	48	4.4	14	2	AAR72903	Aar72903 E. coli p
37	47	4.3	9	3	AAY69963	Aay69963 Human cyc
38	47	4.3	9	4	AAB46947	Aab46947 Human cyc
39	47	4.3	9	7	ADC17709	Adc17709 Modified
40	46	4.2	9	3	AAY69962	Aay69962 Human cyc
41	46	4.2	9	3	AAY69941	Aay69941 Human cyc
42	46	4.2	9	4	AAB46946	Aab46946 Human cyc
43	46	4.2	10	3	AAY69937	Aay69937 Human cyc
44	46	4.2	10	3	AAY69934	Aay69934 Human cyc
45	46	4.2	11	3	AAY69933	Aay69933 Human cyc

ALIGNMENTS

RESULT 1

ABP74769
ID ABP74769 standard; peptide; 14 AA.

XX AC

ABP74769;

XX AC

03-FEB-2003 (first entry)

XX AC

Proteome analysis related peptide #54.

XX AC

Proteome analysis; isolation; determination; diagnostic assay; detection;

KW AC

Protein marker; identification; metastatic; invasive cancer;

KW AC

differential expression; signalling pathway; chromatography.

XX AC

Homo sapiens.

OS AC

Synthetic.

XX AC

WO200277016-A2.

XX AC

03-OCT-2002.

XX AC

22-MAR-2002; 2002WO-EP003368.

XX AC

22-MAR-2001; 2001US-0278171P.

PR AC

12-SEP-2001; 2001US-0318749P.

PR AC

20-SEP-2001; 2001US-0323999P.

XX AC

(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX AC

Vandekerckhove J, Gevaert K;

XX AC

WPI; 2003-067379/06.

XX AC

Method for isolation of peptides from complex mixture of peptides

PT AC

involves specific chemical and/or enzymatic alteration of at least one

XX AC

type of peptide.

XX AC

Example 20; Page 141; 193pp; English.

XX AC

The present invention describes a method (M1) for the isolation of a

CC AC

subset of peptides from a protein peptide mixture (P1). M1 involves: (a)

CC AC

separating the protein peptide mixture into fractions of peptides via

CC AC

chromatography; (b) chemically, or enzymatically, or chemically and

CC AC

enzymatically, altering at least one amino acid of at least one of the

CC AC

peptides in each fraction, thereby generating a subset of altered

CC AC

peptides; and (c) isolating the altered (flagged) peptides out of each

CC AC

fraction via chromatography, where the chromatography of steps (a) and

CC AC

(c) is performed with the same type of chromatography. M1 can be used for

CC the isolation and determination of peptides from protein peptide
 CC mixtures. M1 can also be used in diagnostic assays for detection of the
 CC presence, the absence or a variation in expression level of at least one
 CC protein marker or a specific set of proteins indicative of a disease
 CC state. M1 can be used for identifying target proteins present in
 CC metastatic and invasive cancers, in differential expression of proteins
 CC in transgenic mice, identification of proteins that are upregulated or
 CC down regulated in disease tissues, in identification of intracellular
 CC changes in cells with physiological changes such as metabolic shift, in
 CC the identification of biomarkers in cancers and in the identification of
 CC signalling pathways. The method is gel-free methodology for qualitative
 CC and quantitative proteome analysis without the need for multidimensional
 CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
 CC represent peptide sequences used in the exemplification of the present
 CC invention

XX SQ Sequence 14 AA;

Query Match 7.7%; Score 83; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

OY 124 HYGPGVSMANAGK 137
 DB 1 HYGPGVSMANAGK 14
 |||||

RESULT 2
 AAY69925
 ID AAY69925 standard; peptide; 11 AA.

XX AC AAY69925;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #5.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 XX HW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
 XX diagnosis of tumors.

XX PS Claim 4; Page 50; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 11 AA;

Query Match 6.6%; Score 71; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 119 NFKLKHYGPGW 129
 DB 1 NFKLKHYGPGW 11
 |||||

RESULT 3
 AAY69947

ID AAY69947 standard; peptide; 10 AA.

XX AC AAY69947;

XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #27.

XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 XX HW HLA antigen; diagnosis; tumour; therapy.

XX OS Homo sapiens.

XX PN WO9967288-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.

XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX PT Tumor antigen peptides derived from cyclophilin B for treatment and
 XX diagnosis of tumors.

XX PS Claim 4; Page 56; 64pp; Japanese.

XX CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 10 AA;

Query Match 5.8%; Score 63; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 KLKHYGPGWV 130
 DB 1 KLKHYGPGWV 10
 |||||

RESULT 4

ABR84352
 ID ABR84352 standard; peptide; 10 AA.

XX AC ABR84352;

XX DT 06-NOV-2003 (first entry)

XX DE Human CypB HLA-A2 epitope, SEQ ID NO:3.

XX KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
 XX cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
 XX immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
 XX human; human leukocyte antigen; HLA-A2 epitope.

XX OS Homo sapiens.

XX XX

PN JP2002365286-A.

XX 18-DEC-2002.

XX 18-SEP-2001; 2001JP-00283413.

XX 13-NOV-2000; 2000JP-00345094.

XX (ITOY/) ITO Y.

XX WPI; 2003-508315/48.

XX A detection method of antigen specific T-cells, comprises the use of
PT plural antigenic peptides, useful in semi-quantitative determination of
PT cancer specific T-cell frequencies and for monitoring cellular immunity.

PS Example 7; Page 8; 18pp; Japanese.

XX The invention relates to a method for the detection of antigen specific T
CC -cells in a blood sample involving the use of a plurality of antigenic
CC peptides. The method comprises sampling of peripheral blood monocytes;
CC stimulation of the collected peripheral blood monocytes with antigens
CC without direct use of antigen presenting cells; and detection of T-cells
CC specific to the antigen in the stimulated monocytes. The method is
CC particularly used for the detection of cancer as it can be used in semi-
CC quantitative determination of cancer specific T-cells. It can also be
CC used for cancer vaccine therapy for patients with cervical or prostate
CC cancer. The method can additionally be used to monitor of cellular
CC immunity and cancer immune therapy by detection of specific T-cell
CC frequencies. Sequences ABR84350-ABR84365 represent HLA-A2 (human
CC leukocyte antigen) peptides of human origin used in an example from the
CC invention

XX Sequence 10 AA;

Query Match 5.8%; Score 63; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 KLKHYGPGWV 130

Db 1 KLKHYGPGWV 10

RESULT 5

ID AAY69926 standard; peptide; 11 AA.

XX AAY69926;

XX 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #6.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO9967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX

PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.

XX Claim 4; Page 50; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 11 AA;

Query Match 5.8%; Score 63; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.2;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 IYGERPPDENF 120

Db 1 IYGERPPDENF 11

RESULT 6

AAY69924

ID AAY69924 standard; peptide; 11 AA.

XX AC AAY69924;

XX 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #4.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW HLA antigen; diagnosis; tumour; therapy.

XX Homo sapiens.

XX WO9967288-A1.

XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.

XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.

XX (ITOH/) ITOH K.

XX Itoh K, Gomi S;

XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.

XX Claim 4; Page 50; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 11 AA;

Query Match 5.5%; Score 60; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GYKNSKFRV 89

Db 1 GYKNSKFRV 11

RESULT 7

AAV69928
ID AAY69928 standard; peptide; 9 AA.

XX AC AAY69928;
XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #8.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.

XX PN WO9967288-A1.
XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.

XX DT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 51; 64pp; Japanese.
XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 9 AA;
Query Match 5.4%; Score 58; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;

XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 HYGPGWVSM 132
DB 1 HYGPGWVSM 9

RESULT 8

AAV69930
ID AAY69930 standard; peptide; 10 AA.

XX AC AAY69930;
XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #10.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.

XX PN WO9967288-A1.
XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.

RESULT 9

AAV69944
ID AAY69944 standard; peptide; 11 AA.

XX AC AAY69944;
XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #24.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.

XX PN WO9967288-A1.
XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.

XX DT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 52; 64pp; Japanese.
XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 10 AA;
Query Match 5.4%; Score 58; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 21;

XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 152 AAWLDGKHVVF 161
DB 1 AAWLDGKHVVF 10

RESULT 9

AAV69944
ID AAY69944 standard; peptide; 11 AA.

XX AC AAY69944;
XX DT 11-APR-2000 (first entry)

XX DE Human cyclophilin B peptide fragment #24.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.

XX PN WO9967288-A1.
XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.

XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.

XX DT Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 55; 64pp; Japanese.
XX CC This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours

XX SQ Sequence 11 AA;
Query Match 5.3%; Score 57; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 31;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GLFGKTVPKTV 65
 Db 1 GLFGKTVPKTV 11

RESULT 10
 AAY69929
 ID AAY69929 standard; peptide; 10 AA.
 XX AAY69929;
 AC
 XX 11-APR-2000 (first entry)
 DT
 XX Human cyclophilin B peptide fragment #9.
 DE
 XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-JP003360.
 XX
 PR 25-JUN-1998; 98JP-00178449.
 XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Gomi S;
 XX
 DR WPI; 2000-116932/10.
 XX
 PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX
 PS Claim 4; Page 51; 64pp; Japanese.
 XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX
 SQ Sequence 10 AA;

Query Match 5.1%; Score 55; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 FFITTVKTAW 153
 Db 1 FFITTVKTAW 10

RESULT 11
 AAY69943
 ID AAY69943 standard; peptide; 11 AA.
 XX AAY69943;
 AC
 XX 11-APR-2000 (first entry)
 DT
 XX Human cyclophilin B peptide fragment #23.
 DE
 XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.
 XX

PN WO9967288-A1.
 XX
 PD 29-DEC-1999.
 XX
 PF 24-JUN-1999; 99WO-JP003360.
 XX
 PR 25-JUN-1998; 98JP-00178449.
 XX
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Gomi S;
 XX
 DR WPI; 2000-116932/10.
 XX
 PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.
 XX
 PS Claim 4; Page 55; 64pp; Japanese.
 XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX
 SQ Sequence 11 AA;

Query Match 5.1%; Score 55; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RVIFGLFGKTV 61
 Db 1 RVIFGLFGKTV 11

RESULT 12
 ABG67616
 ID ABG67616 standard; peptide; 14 AA.
 XX AC
 AC ABG67616;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human ADPI tryptic digest peptide #325.
 XX
 KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
 KW Alzheimer's disease-associated feature; neuroprotective;
 KW Alzheimer's disease-associated protein isoform; nootropic;
 KW ADPI tryptic digest peptide.
 XX
 OS Homo sapiens.
 XX
 PN WO200246767-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 29-NOV-2001; 2001WO-GB005289.
 XX
 PR 08-DEC-2000; 2000US-0254431P.
 XX
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX
 PI Herath HMAC, Parekh RB, Rohlff C;
 XX
 DR WPI; 2002-508575/54.
 XX
 PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer disease-associated features or Alzheimer
 PT disease-associated protein isoforms in brain tissue from the subject.
 XX
 PS Claim 7; Page 72; 427pp; English.
 XX

CC The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
 CC subject. The method comprises analysing a sample of brain tissue from a
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
 CC disease-associated features (ADFs), whose relative abundance correlates
 CC with the presence, absence, stage or severity of AD and comparing the
 CC abundance of each feature with the abundance of that chosen feature in
 CC brain tissue from persons free from AD. The invention also describes
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
 CC brain tissue. The methods and compositions of the invention are useful
 CC for the screening, diagnosis or prognosis of AD in a subject, for
 CC determining the stage or severity of AD in a subject, for identifying a
 CC subject at risk of developing AD, or for monitoring the effect of therapy
 CC administered to a subject having AD. Antibodies capable of binding to
 CC ADPIs are useful for treating or preventing AD, and for determining the
 CC efficacy of a given treatment regime. An agent that modulates the
 CC activity of ADPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
 CC human ADPI tryptic digest peptides
 XX
 SQ Sequence 14 AA;

Query Match 5.0%; Score 54; DB 5; Length 14;
 Best Local Similarity 71.4%; Pred. No. 89;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 88 VIKDFMIQGGDFTR 101
 :||| |||||
 Db 1 IIPGFMCGGDFTR 14

RESULT 13
 ID ADA23735
 ADADA23735 standard; peptide; 14 AA.
 XX
 AC ADA23735;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Alzheimer's disease-associated protein isoform tryptic peptide #344.
 XX
 KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
 KW Alzheimer's disease-associated protein isoform; ADPI.
 XX
 OS Homo sapiens.

XX US2003064411-A1.
 XX 03-APR-2003.
 XX 10-DEC-2001; 2001US-00014340.
 XX 08-DEC-2000; 2000US-0254431P.

XX (HERA/) HERATH H M A C.
 XX (PARE/) PAREKH R B.
 XX (ROHL/) ROHLFF C.

XX Herath H M A C, Parekh R B, Rohlf C;
 XX WPI; 2003-540784/51.

XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT involves analyzing test sample of brain tissue from subject, and
 PT comparing feature in test sample with that of person(s) free from
 PT Alzheimer's disease.

XX Disclosure; SEQ ID NO 344; 115pp; English.

XX The invention relates to a method of screening or diagnosing Alzheimer's
 CC disease in a subject. The method is useful for screening, diagnosis or
 CC prognosis of Alzheimer's disease in a subject for determining the stage

CC of severity of Alzheimer's disease in a subject, for identifying a
 CC subject at risk of developing Alzheimer's disease, or for monitoring the
 CC effect of therapy administered to a subject having Alzheimer's disease.
 CC The method is also useful in treating vascular dementia, Lewy body
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
 CC depression. The inventive method identifies sensitive and specific
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
 CC It provides therapeutic agents for Alzheimer's disease that works
 CC quickly, potentially, specifically with fewer side effects. The present
 CC sequence represents the amino acid sequence of a Alzheimer's disease-
 CC associated protein isoform tryptic peptide.

XX Sequence 14 AA;

Query Match 5.0%; Score 54; DB 6; Length 14;
 Best Local Similarity 71.4%; Pred. No. 89;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 88 VIKDFMIQGGDFTR 101
 :||| |||||
 Db 1 IIPGFMCGGDFTR 14

RESULT 14
 ID AAY69949 standard; peptide; 10 AA.
 XX
 AC AAY69949;
 XX

XX 11-APR-2000 (first entry)
 XX Human cyclophilin B peptide fragment #29.

XX Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KW HLA antigen; diagnosis; tumour; therapy.
 XX
 OS Homo sapiens.

XX WO9967288-A1.
 XX 29-DEC-1999.

XX 24-JUN-1999; 99WO-JP003360.
 XX 25-JUN-1998; 98JP-00178449.

XX (SUMU) SUMITOMO PHARM CO LTD.
 XX (ITO/) ITOH K.

XX Itoh K, Gomi S;
 XX WPI; 2000-116932/10.

XX Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.

XX Claim 4; Page 57; 64pp; Japanese.

XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumour antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours

XX Sequence 10 AA;

Query Match 4.9%; Score 53; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 FITTVKTAWL 154
 :||| |||||
 Db 1 FITTVKTAWL 10

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RESULT 15
AAV69945
ID AAV69945 standard; peptide; 10 AA.
XX
AC AAV69945;
XX
11-APR-2000 (first entry)
XX
Human cyclophilin B peptide fragment #25.
DE
Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW
HLA antigen; diagnosis; tumour; therapy.
XX
Homo sapiens.
OS
WO9967288-A1.
PN
29-DEC-1999.
PD
24-JUN-1999; 99WO-JP003360.
PF
25-JUN-1998; 98JP-00178449.
PR
(SUMU ) SUMITOMO PHARM CO LTD.
PA
(ITOH/) ITOH K.
XX
Itoh K, Gomi S;
PI
WPI; 2000-116932/10.
DR
Tumor antigen peptides derived from cyclophilin B for treatment and
DE
diagnosis of tumors.
PT
Claim 4; Page 56; 64pp; Japanese.
PS
This sequence represents a cyclophilin B peptide of the invention. The
CC
peptides are tumour antigen peptides derived from cyclophilin B, that
CC
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC
peptides are used for the treatment and diagnosis of tumours
XX
Sequence 10 AA;
SQ
Query Match 4.8%; Score 52; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 60 TVPKTVDNFV 69
Db 1 TVPKTVDNFV 10
XX
RESULT 16
AAV69923
ID AAV69923 standard; peptide; 9 AA.
XX
AC AAV69923;
XX
11-APR-2000 (first entry)
XX
Human cyclophilin B peptide fragment #3.
DE
Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW
HLA antigen; diagnosis; tumour; therapy.
XX
Homo sapiens.
OS
WO9967288-A1.
PN
29-DEC-1999.
PD
24-JUN-1999; 99WO-JP003360.
PF
XX

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PR 25-JUN-1998; 98JP-00178449.
XX
(SUMU ) SUMITOMO PHARM CO LTD.
PA
(ITOH/) ITOH K.
XX
Itoh K, Gomi S;
PI
WPI; 2000-116932/10.
DR
Tumor antigen peptides derived from cyclophilin B for treatment and
DE
diagnosis of tumors.
PT
Claim 4; Page 50; 64pp; Japanese.
PS
This sequence represents a cyclophilin B peptide of the invention. The
CC
peptides are tumour antigen peptides derived from cyclophilin B, that
CC
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC
peptides are used for the treatment and diagnosis of tumours
XX
Sequence 9 AA;
SQ
Query Match 4.7%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 77 GFGYKNSKF 85
Db 1 GFGYKNSKF 9
XX
RESULT 17
AAV69955
ID AAV69955 standard; peptide; 11 AA.
XX
AC AAV69955;
XX
11-APR-2000 (first entry)
XX
Human cyclophilin B peptide fragment #35.
DE
Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW
HLA antigen; diagnosis; tumour; therapy.
XX
Homo sapiens.
OS
WO9967288-A1.
PN
29-DEC-1999.
PD
24-JUN-1999; 99WO-JP003360.
PF
25-JUN-1998; 98JP-00178449.
PR
(SUMU ) SUMITOMO PHARM CO LTD.
PA
(ITOH/) ITOH K.
XX
Itoh K, Gomi S;
PI
WPI; 2000-116932/10.
DR
Tumor antigen peptides derived from cyclophilin B for treatment and
DE
diagnosis of tumors.
PT
Claim 4; Page 58; 64pp; Japanese.
PS
This sequence represents a cyclophilin B peptide of the invention. The
CC
peptides are tumour antigen peptides derived from cyclophilin B, that
CC
recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC
peptides are used for the treatment and diagnosis of tumours
XX
Sequence 11 AA;
SQ
Query Match 4.7%; Score 51; DB 3; Length 11;

```

Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 VLEGMEVVRKV 174
Db 1 VLEGMEVVRKV 11

RESULT 18
AAY69922
ID AAY69922 standard; peptide; 9 AA.
XX AC
XX AAY69922;
XX DT 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #2.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.
XX EN WO9967288-A1.
XX FN 29-DEC-1999.
XX PD 24-JUN-1999; 99WO-JP003360.
XX PF 25-JUN-1999;
XX PR 25-JUN-1998; 98JP-00178449.
XX XX (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.
XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.
XX DE Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 49; 64pp; Japanese.
XX OS This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours
XX SQ Sequence 9 AA;
Query Match 4.6%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 DFMTQGGDF 99
Db 1 DFMTQGGDF 9

RESULT 19
AAY69927
ID AAY69927 standard; peptide; 9 AA.
XX AC
XX AAY69927;
XX DT 11-APR-2000 (first entry)
XX DE Human cyclophilin B peptide fragment #7.
XX KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX KW HLA antigen; diagnosis; tumour; therapy.
XX OS Homo sapiens.

XX WO9967288-A1.
XX PD 29-DEC-1999.
XX PF 24-JUN-1999; 99WO-JP003360.
XX PR 25-JUN-1998; 98JP-00178449.
XX XX (SUMU) SUMITOMO PHARM CO LTD.
XX PA (ITOH/) ITOH K.
XX PI Itoh K, Gomi S;
XX DR WPI; 2000-116932/10.
XX DE Tumor antigen peptides derived from cyclophilin B for treatment and
XX PT diagnosis of tumors.
XX PS Claim 4; Page 51; 64pp; Japanese.
XX OS This sequence represents a cyclophilin B peptide of the invention. The
XX CC peptides are tumour antigen peptides derived from cyclophilin B, that
XX CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX CC peptides are used for the treatment and diagnosis of tumours
XX SQ Sequence 9 AA;
Query Match 4.6%; Score 50; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 RFPDENFKL 122
Db 1 RFPDENFKL 9

RESULT 20
AAB46931
ID AAB46931 standard; peptide; 9 AA.
XX AC AAB46931;
XX DT 04-MAY-2001 (first entry)
XX DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 17.
XX KW Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
XX KW virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
XX KW viral infectious disease; cyclophilin B; human.
XX OS Homo sapiens.
XX EN EP1074267-A1.
XX PD 07-FEB-2001.
XX PF 24-JUL-2000; 2000EP-00306263.
XX PR 22-JUL-1999; 99JP-00207687.
XX PA (SUMU) SUMITOMO PHARM CO LTD.
XX PI Takasu H, Gotoh M, Yamaoka T;
XX DR WPI; 2001-193144/20.
XX PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
XX PT the manufacture of an agent for the induction of antigen-specific T
XX PS cells.
XX PS Disclosure; Page 15; 25pp; English.
XX